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Subject:

Hamud, Fozia
Wednesday, February 27, 2002 8:47 AM
STIC-Biotech/ChemLib
search for 09/617,720

Please search SEQ ID NO:1 from 310 to 2562 against commercial data bases and interference data bases. Thanks.

Fozia Hamud
Art Unit 1647
Crystal-Mall-One, Room 10Bo5
308-8891
mail Box: CM110C01

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2002, 10:36:04 ; Search time 1672.78 Seconds

(without alignments)
2219.387 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
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Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

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1: gb_ba: *
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34: em_htg_inv: *
35: em_htg_rod: *
36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	2253	100.0	2563	6	AX080389 Sequence
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3	2241	99.5	2613	9	HA242737 Homo sapi
4	2205.2	97.9	2598	6	AX092420 Sequence
5	2195.6	97.5	6540	6	AX080431 Sequence
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8	2180.4	96.8	7604	9	AF216693 Homo sapi
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10	2178.4	96.7	2648	6	AX069309 Sequence
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12	1835	81.4	1866	9	AK002125 Homo sapi
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15	886.2	39.3	985	6	AX069305 Sequence
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ACCESSION	AX080389.1	GI:13159840				
VERSION						
KEYWORDS						
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		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE		1 (bases 1 to 2563)				
AUTHORS		Nicklin,M. and Barton,J.				
TITLE		The 11-111 gene and polypeptide products				
JOURNAL		Patent: WO 0105974-A 1 25-JAN-2001;				
		Interleukin Genetics, Inc. (US)				
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DESCRIPTION		Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L gene) transcript 2.	
ACCESSION	AJ242738.1	GI:6165335	
VERSION	AJ242738.1	GI:6165335	
KEYWORDS	IL1L gene; interleukin-1-like protein 1.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Barton,J.,L., Herdset,R., Bosio,D., Higgins,L. and Nicklin,M.J.		
TITLE	A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities		
JOURNAL	Eur. J. Immunol. 30(11), 3299-3308 (2000)		
MEDLINE	20545212		
REFERENCE	2 (bases 1 to 2604)		
NICKLIN,M.J.			
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield, S10 2UF, UNITED KINGDOM		
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DEFINITION	Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L1 gene), transcript 1.		02-NOV-2000
ACCESSION	AJ242737		
VERSION	AJ242737.1	GI:6165333	
KEYWORDS	IL1L1 gene; Interleukin-1-like protein-1.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2613)		
TITLE	Barton, J.L., Herbs, R., Bostio, D., Higgins, L. and Nicklin, M.J.		
JOURNAL	A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities		
MEDLINE	Eur. J. Immunol. 30 (11), 3299-3308 (2000)		
REFERENCE	20545212		
AUTHORS	2 (bases 1 to 2613)		
TITLE	Nicklin, M.J.		
JOURNAL	Direct Submission		
FEATURES	Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM		
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RESULT 4
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LOCUS AX092420
DEFINITION Sequence 151 from Patent WO0116318.
ACCESSION AX092420
VERSION AX092420.1 GI:13444524
KEYWORDS human.
SOURCE

REFERENCE	ORGANISM	TITLE
AUTHORS	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2598) Eaton,D.L., Flivaroff,E., Gertlisen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Matanabe,C.K. and Wood,W.I.	Secreted and transmembrane polypeptides and nucleic acids encoding the same the same Patent: WO 0116318-A 151 08-MAR-2001; Genentech, Inc. (US)
FEATURES	source location/Qualifiers 1..2598 /organism="Homo sapiens" /db_xref="taxon:9606"	
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Query Match	97.9%; Score 2205.2; DB 6; Length 2598;	
Best Local Similarity	99.5%; Pred. No. 0;	
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407	CTGCGTACCGGGGCGGTGTTCTCTGTGACGCGTCCCTGAAGCCGATCAGCTCTGACGTCA 466	
121	cccaagctcccggaatgctgctgtaagctgaccccaacacagacttcaactccaagcagt 180	
467	CCCAAGCTTCCCGGAATGCTGCTGGAATGCCCCCATCAGACACTTCCTACCTCCAGCAGT 526	
181	gtacactgggcaacgctgccccccgaactccctctggagagagcaagctcgggtgagaggtc 240	
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241	gagctgagagagaccatctgacgaacaaactcttctctctcaagagcccccaagctctga 300	
586	GAGTGGAGAGAGACCCATGAGGGAGCAATCACTCTCTCTGCTCAGAGACCCCAAGCTCTGA 645	
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766	ACCATGTGGGGGTAACTCGGGAATTAACATATAAAGATTCTGTGGGGGGTGGGGAG 825	
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RESULT 5

AX080431 6540 bp DNA PAT 22-FEB-2001
LOCUS AX080431
DEFINITION Sequence 43 from Patent WO0105974.
ACCESSION AX080431
VERSION AX080431.1 GI:13159871
KEYWORDS

SOURCE

human.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 6540)

AUTHORS Nicklin,M. and Barton,J.

JOURNAL The 11-111 gene and polypeptide products

Patent: WO 0105974-A 43 25-JAN-2001.

INTERLEUKIN 11-111 GENE AND POLYPEPTIDE PRODUCTS

Interleukin Genetics, Inc. (US)

Location/Qualifiers

1. 6540

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 1747 a 1458 c 1709 g 1626 t

ORIGIN

Query Match 97.5%; Score 2195.6; DB 6; Length 6540;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 2237; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

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RESULT 6
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LOCUS Homo sapiens IL1L1 gene for interleukin-1 like protein 1, exons
DEFINITION 1-6.
ACCESSION AJ271338
VERSION AJ271338.1 GI:6729586
KEYWORDS IL1L1 gene; Interleukin-1 like protein 1.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 6540)
AUTHORS Barton,J.L., Herbst,R., Bosisio,D., Higgins,L. and Nicklin,M.J.
TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)
MEDLINE 20545212
REFERENCE 2 (bases 1 to 6540)
AUTHORS Nicklin,M.J.H.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
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BASE COUNT 1747 a 1458 c 1709 g 1626 t
ORIGIN

Query Match 97.5%; Score 2195.6; DB 9; Length 6540;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2237; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

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	ORGANISM	Homo sapiens			

REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Homnidae; Homo.
1 (bases 1 to 197308)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 197308)
Waterston, R.H.
Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington

REFERENCE 3 (bases 1 to 197308)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2001) Genome Sequencing Center, Washington

ENT On Jul 14, 2001 this sequence version replaced gl:13431151.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WGS05C
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: H.NH0339F22

FEATURES	Location/Qualifiers
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Query Match	97.2%	Score 2189.2;	DB 9;	Length 197308;
Best Local Similarity	99.1%;	Pred. No. 0;		
Matches 2233;	Conservative	0;	Mismatches 18;	Indels 3; Gaps 3

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DEFINITION gene, complete cds.
ACCESSION AF216693
VERSION AF216693.1 GI:8572054
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 7604)
Muller, J.J., Nelken, S.T. and Ford, J.E.
Organization of the human Interleukin-1 receptor antagonist gene
IL1HY1
JOURNAL Immunogenetics 51 (6), 425-428 (2000)
MEDLINE 20322477
REFERENCE 2 (bases 1 to 7604)
Muller, J.J., Nelken, S.T. and Ford, J.E.
Direct Submission
Submitted (15-DEC-1999) Functional Genomics, HYSEQ Inc, 670 Almanor
Ave., Sunnyvale, CA 94086, USA
JOURNAL Location/Qualifiers
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DEFINITION Sequence 8 from Patent WO0102571.
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VERSION AX069311.1 GI:12579183
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 7605)
AUTHORS Ford, J. and Pace, A.
TITLE A interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 8 11-JAN-2001;
HISQ, INC. (US)
FEATURES
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VERSION	AX069309.1				
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 2648)				
JOURNAL	Ford, J. and Pace, A.				
FEATURES	A interleukin-1 receptor antagonist and uses thereof				
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REFERENCE
AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R.,
Drmanac,R. and Ford,J.E.
TITLE IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene
JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)
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TITLE Direct Submission
JOURNAL Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670
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ACCESSION	AK002125			
VERSION	AK002125.1	GI:7023811		
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AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Hominoidee: Homo.			
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	Nishikawa,T., Negai,K., Sugano,S., Shiratori,A., Sudo,H.,			
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	Ishii,S., Kawai,Y., Saito,K., Yamamoto,D., Wakamatsu,A.,			
	Nakamura,Y., Nishihari,K., Masuo,Y., Niinomiya,K. and Iwayanagi,T.			
	NEDO human cDNA sequencing project			
TITLE				

JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 1866)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yama, Kisaizaki, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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ORGANISM	Homo sapiens		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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JOURNAL	Ford, J. and Pace, A.		
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2180.4	96.8	7605	22	AAE31356 Extension of genom
6	2178.4	96.7	2647	22	AAE31354 Extension of B2HFL
7	2178.4	96.7	2648	20	AAZ30051 cDNA encoding a hu
8	2020.6	89.7	2490	21	AAZ50813 Human TANGO-93 cDN
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11	1566.6	69.5	5752	20	AAZ30052 DNA encoding a hum

12	933.2	41.4	1323	21	AAZ50812 Human TANGO-93 cDN
13	886.2	39.3	985	22	AAE31352 B2HFLS20W cDNA 11b
14	886.2	39.3	1282	22	AAE31353 Extension of B2HFL
15	885.2	39.3	1282	20	AAZ30050 cDNA encoding a hu
16	883.6	39.2	985	20	AAZ30049 cDNA encoding a hu
17	641	28.5	1025	22	AAAD12295 Human Interleukin-
18	527.8	23.4	555	22	AAH07999 Human cDNA clone (
19	380.8	16.9	416	22	AAH12965 Human cDNA clone (
20	354.6	15.7	766	21	AAA09193 Human IL-1 homolo
21	230	10.2	357	22	AAE31351 B2HFLS20W cDNA 11b
22	222.8	9.9	358	20	AAZ30048 cDNA encoding a hu
23	188	8.3	468	20	AAH89432 Human Interleukin
24	188	8.3	468	21	AAAS1597 Human IL-1 recepto
25	159.2	7.1	475	22	AAI05083 Probe #5074 used t
26	156.4	6.9	1275	21	AAA09198 Murine IL-1 homolo
27	156.4	6.9	1284	22	AAE27924 Murine IL-1L1 codi
28	156.4	6.9	1360	21	AAZ50811 Murine TANGO-93 cD
29	156.4	6.9	1385	21	AAAS1599 Murine IL-1 recept
30	154.8	6.3	8032	22	AAE31372 Invention related
31	141.6	6.3	468	22	AAE31373 Murine Interleukin
32	141.6	6.3	468	22	AAE31373 Murine Interleukin
33	140.6	6.2	470	19	AAV71958 Rodent Interleukin
34	138.6	6.2	468	20	AAH89431 Mouse Interleukin
35	135	6.0	465	21	AAA09194 Human IL-1 homolo
36	132.2	5.9	465	21	AAA09195 Human IL-1 homolo
37	128	5.7	590	22	AAI19031 Probe #8964 for ge
38	128	5.7	590	22	AAI14171 Probe #12857 used
39	125	5.5	936	22	AAE58252 Oligonucleotide D1
40	125	5.5	936	22	AAE58254 Oligonucleotide D1
41	125	5.5	936	22	AAE58257 Oligonucleotide D1
42	125	5.5	936	22	AAE58259 Oligonucleotide D2
43	125	5.5	936	22	AAE58262 Oligonucleotide D2
44	125	5.5	938	22	AAE58255 Oligonucleotide D1
45	123.6	5.5	1731	20	AAZ98008 Human secreted pro

ALIGNMENTS

RESULT 1	
AAE27921	
ID	AAE27921 standard; cDNA; 2562 BP.
XX	
AC	AAE27921:
XX	
DT	08-MAY-2001 (first entry)
XX	
DE	Human IL-1L1 coding sequence.
XX	
KW	Human: IL-1L1; Interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW	chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW	rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW	osteoporosis; systemic lupus erythematosus; ss.
XX	
OS	Homo sapiens.
XX	
PH	
FT	key
FT	Location/Qualifiers
FT	30..497
FT	/tag= a
FT	/product= "IL-1L1"
FT	/note= "this region is specifically claimed"
XX	
PN	WO200105974-A2.
XX	
PD	25-JAN-2001.
XX	
XX	
PF	17-JUL-2000; 2000MO-US19508.
XX	
XX	
PR	16-JUL-1999; 99US-0144298.
XX	
PA	(INTE-) INTERLEUKIN GENETICS INC.
XX	
PI	Nicklin M, Barton J;

XX WPI: 2001-091974/10.

XX Nucleic acids encoding human and murine interleukin-1L1 polypeptides
PT useful for controlling inflammatory processes -
XX
PS Claim 12: Fig 1: 150pp: English.

CC The present invention provides the protein and coding sequences of the
CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
CC located between the IL-1beta and IL-1receptor genes at human chromosome
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
CC of heart disease, cancer and inflammatory diseases such as Rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
CC severe periodontal disease and pregnancy complications. The present
CC sequence is the human IL-1L1 coding sequence.

XX Sequence 2562 BP: 678 A: 579 C: 635 G: 670 T: 0 other:

● Very Match 100.0%: Score 2253: DB 22: Length 2562:
● Best Local Similarity 100.0%: Pred. No. 0:
Matches 2253: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 aatccaagagctcaactcttaccgagcgagacatgaggctcaactccagctcgatcg 60
DB 310 aatccaagagctcaactcttaccgagcgagacatgaggctcaactccagctcgatcg 369
QY 61 ctgctaccgagctggtctctctgtagcaagtgctgtagaagccgacatgagctcgaactca 120
DB 370 ctgctaccgagctggtctctctgtagcaagtgctgtagaagccgacatgagctcgaactca 429
QY 121 ccaagctcccgagagatgctgtagaagtgcccccacacagactcttaccgagcagt 180
DB 430 ccaagctcccgagagatgctgtagaagtgcccccacacagactcttaccgagcagt 489
QY 181 gtgactaaggagcaagctgccccccagaaactccctgtagcagagccagctcggtgaggggt 240
DB 490 gtgactaaggagcaagctgccccccagaaactccctgtagcagagccagctcggtgaggggt 549
QY 241 gagtgagagagacacatgtaggagacatcaactcttctgctctcagagcccccagctcga 300
DB 550 gagtgagagagacacatgtaggagacatcaactcttctgctctcagagcccccagctcga 609
QY 301 cttagtgagcagctgacacacttgctctctgtagtccagcttgtagaattctgagatt 360
DB 610 cttagtgagcagctgacacacttgctctctgtagtccagcttgtagaattctgagatt 669
QY 361 ggaagctcaagctcagaggtctcccccacatgtagttagtctgtagaacttgtaaaa 420
DB 670 ggaagctcaagctcagaggtctcccccacatgtagttagtctgtagaacttgtaaaa 729
QY 421 accgtctgaggtagaactgtagaatacagtaaaagattctctgtaggggtgaggaggag 480
DB 730 accgtctgaggtagaactgtagaatacagtaaaagattctctgtaggggtgaggaggag 789
QY 481 tgcctgagataatctctgtagaactgtagaagtgtagaagcttgtagaagcttgtagaagc 540
DB 790 tgcctgagataatctctgtagaactgtagaagtgtagaagcttgtagaagcttgtagaagc 849
QY 541 aaccatccacagctgtagaactttagaggttagagcttccacatgaaagctctctacac 600
DB 850 aaccatccacagctgtagaactttagaggttagagcttccacatgaaagctctctacac 909
QY 601 accactgtgcagagagagaggtgtagtaagtagcagagacatagtcgctctgagccagc 660
DB 910 accactgtgcagagagagaggtgtagtaagtagcagagacatagtcgctctgagccagc 969
QY 661 cccacccctctctcttctgtagcagctgtagaagtgtagaagcttctctctctcccca 720
DB 970 cccacccctctctcttctgtagcagctgtagaagtgtagaagcttctctctctcccca 1029

QY 721 tcatctgtctgtagcagtagagaggtgtagtctcagagaagaatggtctgagctcagaag 780
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QY 781 ataaagataagtagagtagtagtctctctctttaaataaaccagaatacaataatcc 840
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DB 1150 cagaagctggtctctatctccatgtaaaagtgtctcagatgacatgtagaagaagcacta 1209
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DB 1330 ggtgatttctctttaaattcgttaattatctgtagtcttcttcttcttctcacaatgag 1389
QY 1081 atgaattctctgtataaataaataaagaagaataatcatctgaggtgaagcagagacat 1140
DB 1390 atgaattctctgtataaataaataaagaagaataatcatctgaggtgaagcagagacat 1449
QY 1141 catctctgattgtctcagctcagctcccaattcccccagagtaaatcttaattgtagagctct 1200
DB 1450 catctctgattgtctcagctcagctcccaattcccccagagtaaatcttaattgtagagctct 1509
QY 1201 gctgctctggtctggtgtagtagtagatcaggaagaacatcccaagaagaagcagtagag 1260
DB 1510 gctgctctggtctggtgtagtagtagatcaggaagaacatcccaagaagaagcagtagag 1569
QY 1261 gaagctgtgctgaggtctgtagtctgtagaactctgtagtaaggaacttaagaacaaaat 1320
DB 1570 gaagctgtgctgaggtctgtagtctgtagaactctgtagtaaggaacttaagaacaaaat 1629
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DB 1750 ggaatctcagctgtgaggttattctgtagaataaaggtctcctgtagttagttagaaga 1809
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DB 1870 aggaagagacacagagacagagagagacgaggaagacatgtagaagaatgaagcagaga 1929
QY 1621 tggagattctgtagcagcacaagcttagaagaacacaaagattgtgtagcaacatcagaagctt 1680
DB 1930 tggagattctgtagcagcacaagcttagaagaacacaaagattgtgtagcaacatcagaagctt 1989
QY 1681 ggaagagagcagaagaagaattctctctgtagaggtttagaaggtatagaagctctgtagaa 1740
DB 1990 ggaagagagcagaagaagaattctctctgtagaggtttagaaggtatagaagctctgtagaa 2049
QY 1741 ccttaattcagagcttccagctcctgtagaagaaagaagaagaataaattctgtagctttagaa 1800
DB 2050 ccttaattcagagcttccagctcctgtagaagaaagaagaagaataaattctgtagctttagaa 2109
QY 1801 ccaccaagataattggttagacagagcttaggaataataacacagctgtagaataatgctc 1860

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|||||
Db 2110 ccaccagagataatcgtttacagcagctctaggaactatacagctgcttaaatatcc 2169
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Db 2170 cgtctcctcgtgttaacttctgtgtgtgtccctcccaaatatgataagttgctt 2229
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Db 2230 tctgaccatagataatgacgaagtgatgcatgacatccatccaaagtataataa 2289
Oy 1981 agacactgacgttctacttgagccctctctctctgcccacacgcccccatctatc 2040
Db 2280 agacactgacgttctacttgagccctctctctctgcccacacgcccccatctatc 2349
Oy 2041 tggctcactcgtctcgtggggaagcagctgcatgcatatgacgaggtataagagact 2100
Db 2350 tggctcactcgtctcgtggggaagcagctgcatgcatatgacgaggtataagagact 2409
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Db 2530 gacgaataatgataataatgacgagagaagag 2562

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RESULT 2

AAE92133 standard; cDNA; 2598 BP.

AAE92133;

15-MAY-2001 (first entry)

Human PRO342 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US23328.

01-SEP-1999; 99WO-US20111.

15-SEP-1999; 99WO-US21090.

07-DEC-1999; 99US-0169495.

09-DEC-1999; 99US-0170262.

11-JAN-2000; 2000US-0175481.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04342.

03-MAR-2000; 2000WO-US04414.

25-APR-2000; 2000US-0187202.

22-MAY-2000; 2000WO-US14042.

05-JUN-2000; 2000US-0209832.

(GETH) GENENTECH INC.

Eaton DJ, Flivareoff E, Gerritsen ME, Goddard A, Godowski PJ,

Grimaldi CJ, Gurney AL, Watanabe CK, Wood WT.

WPI: 2001-183260/18.

P-PSDB: AAB87601.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Claim 2: Fig 151; 278pp; English.

The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 other;

Query Match 97.9%; Score 2205.2; DB 22; Length 2598;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

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Db 467 cccagcttccgagaaatgtgtcgtgaaagcccccacacacatctacttccagcagt 526
Oy 181 gtcactaaggagcaagctgcccccccaagaactccctgagcagagcagctggggtgaa 240
Db 527 gtcactaaggagcaagctgcccccccaagaactccctgagcagagcagctggggtgaa 585
Oy 241 gagtggagagagaccacatgagcagaacatcctcttctgctcgaagaccccgagtcga 300
Db 586 gagtggagagagaccacatgagcagaacatcctcttctgctcgaagaccccgagtcga 645
Oy 301 cttagtgggacacttgacacacttcttctgtgttcccaatttgacaaattctggaatt 360
Db 646 cttagtgggacacttgacacacttcttctgtgttcccaatttgacaaattctggaatt 705
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Db 706 ggaagctcaatcagaagctctcccccacatgagtgatgctcgtggaacctgtgaa 765
Oy 421 accatgtgggttaaacctgaggaaatacagaaagattctgtgagggtgagggtgagg 480
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Db 886 aaccacatcccaatgagcttaataagtgatgagtcctccacatgaaatccctcacc 945
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Db 1006 cccaccccttccctt-attctgacactgtatagtaacttcttcttccctcc 1065
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|||||
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Db 1366 aggtgattctctttaaattcgttaatttaattcgtatcttcccaattcttcaatgaa 1425
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Db 1426 gatgaattcctctgtaaaaaaagaagaataatbaatcttgaggtgaagcagagcagaca 1485
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Db 1486 tcatctctgattgtctcgaagctcccaattcccgaggttaaaattgaatcgaatctt 1545
Qy 1200 tgcgtgctctgtgtgtgtgtatgtatcagaagaacagatcagcaaaagccactgaga 1259
Db 1546 tgcgtgctctgtgtgtgtgtatgtatcagaagaacagatcagcaaaagccactgaga 1605
Qy 1260 ggaagctgtgctggaattgtgtgtgtgaatctctgtgtgaaggaacttaagaacaaa 1319
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Db 1726 agtctcctaagaagcgtgctgtatgtatgtgaattgtgtccctcctaattacacacctt 1785
Qy 1440 tggaaatccagctgtgtgtatctatcttgagaataagctctgcagatgtatgtatga 1499
Db 1786 tggaaatccagctgtgtgtatctatcttgagaataagctctgcagatgtatgtatga 1845
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Db 1846 acaagatcagctgtgtgaagtagaacttaattcaatagcaggttccctgtatgaa 1905
Qy 1560 aaggaagaagacacagacagagagacgcgaggagaagactatgtaaaagtgaagcagag 1619
Db 1906 aaggaagaagacacagacagagagacgcgaggagaagactatgtaaaagtgaagcagag 1965
Qy 1620 atcgaagtttgcagcccaagctaaagaacacaaagatgtgcacaatcagaagct 1679
Db 1966 atcgaagtttgcagcccaagctaaagaacacaaagatgtgcacaatcagaagct 2025
Qy 1680 tggaaagagcaagaagaatcttccctcagaagcttgaagaggaatacgcgtcgtcgaa 1739
Db 2026 tggaaagagcaagaagaatcttccctcagaagcttgaagaggaatacgcgtcgtcgaa 2085
Qy 1740 acctaatctcagactccagcctctgaaacgaagaagaataattcggctgttttaa 1799
Db 2086 acctaatctcagactccagcctctgaaacgaagaagaataattcggctgttttaa 2145
Qy 1800 gccaccaaggaataattgtttacagagctctagaagaataataagctgtcctaaatgatc 1859
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Db 2146 gccaccaaggaataattgtttacagagcctctagaagaactaatacagctgtcctaaatgatc 2205
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Db 2206 cctgtctcctcgtgttttaacattctgtgtgtccctcccaacatgttaaccaagtgtct 2265
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Db 2266 ttgtgacccaaataagatagtcagaagtcagatgcagtcacactcacaagataagttataa 2324
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Db 2325 aagaacatgcagcttctacttgaagcctctctctctgcacacacgcgcccaatctatc 2384
Qy 2040 ttggtcactcgtctcgtgggaagctagctgcacatctatgaacagagcctataagaagac 2099
Db 2385 ttggtcactcgtctcgtgggaagctagctgcacatctatgaacagagcctataagaagac 2444
Qy 2100 ttacgtgttaaaaaatgaagctctctgcacacagccacatgaatgaacctagaagcagag 2159
Db 2445 ttacgtgttaaaaaatgaagctctctgcacacagccacatgaatgaacctagaagcagag 2504
Qy 2160 actcgtgagataatcgatgtttgtgttttaagtgtgctcagtttgcgtctaactgtta 2219
Db 2505 actcgtgagataatcgatgtttgtgttttaagtgtgctcagtttgcgtctaactgtta 2564
Qy 2220 tgcagcaatagataaataatgcagagaagag 2253
Db 2565 tgcagcaatagataaataatgcagagaagag 2598
|||||
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RESULT 3

AAF27950
ID AAF27950 standard; DNA; 6540 BP.

AAF27950:

08-MAY-2001 (first entry)

Interleukin-IL1 genomic sequence.

Human: IL-1L1; Interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
Chromosome 2q13; Inflammatory disease; heart disease; Graves' disease;
Rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
osteoporosis; systemic lupus erythematosus; ds.

Unidentified.

WO200105974-A2.

25-JAN-2001.

17-JUL-2000; 2000WO-US19508.

16-JUL-1999; 99US-0144298.

(INTE-) INTERLEUKIN GENETICS INC.

Nicklin M, Barton J;

WPI: 2001-091974/10.

Nucleic acids encoding human and murine interleukin-1L1 polypeptides
useful for controlling inflammatory processes -

Examples; Fig 11: 150pp; English.

The present invention provides the protein and coding sequences of the
human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
located between the IL-1beta and IL-1receptor genes at human chromosome
2q13. The sequences are useful in the diagnosis, prevention and treatment
of heart disease, cancer and inflammatory diseases such as rheumatoid
arthritis, systemic lupus erythematosus, inflammatory bowel disorder,

CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
CC severe periodontal disease and pregnancy complications. The present
CC sequence is the IL-1L1 gene.
XX

Sequence 6540 BP; 1747 A; 1458 C; 1709 G; 1626 T; 0 other:

Query Match 97.5%; Score 2195.6; DB 22; Length 6540;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2237; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

QY 1 aatcaagaagcttcaacctctacacgacggaatgagggctcacccacagcttcagatcgg 60
DB 4271 aatcaagaagcttcaacctctacacgacggaatgagggctcacccacagcttcagatcgg 4330
QY 61 ctgcttaccgggctcgtct 120
DB 4331 ctgcttaccgggctcgtct 4390
DB 121 cccagcttcccgagaatggtgtgtgaaatgccccacacacacacacacacacacacac 180
DB 4391 cccagcttcccgagaatggtgtgtgaaatgccccacacacacacacacacacacacac 4450
QY 181 gtaactaaggacacg tgcctcccccacgaactcccttgagcagagccagctcgaagggt 240
DB 4451 gtaactaaggacacg tgcctcccccacgaactcccttgagcagagccagctcgaagggt 4509
QY 241 gagtggagaagacacacatgagcgaacacacacacacacacacacacacacacacac 300
DB 4510 gagtggagaagacacacatgagcgaacacacacacacacacacacacacacacacac 4569
QY 301 cttaagtggac 360
DB 4570 cttaagtggac 4629
QY 361 ggaagctcagctcagcaggtccctcccccacagctgagctcgtctgagacacacacac 420
DB 4630 ggaagctcagctcagcaggtccctcccccacagctgagctcgtctgagacacacacac 4689
QY 421 accatgctgggtgtaaacctcgggaataacacacacacacacacacacacacacacac 480
DB 4690 accatgctgggtgtaaacctcgggaataacacacacacacacacacacacacacacac 4749
QY 481 tgcctgggaatcctcctgtttaaagtaacacacacacacacacacacacacacacac 540
DB 4750 tgcctgggaatcctcctgtttaaagtaacacacacacacacacacacacacacacac 4809
DB 541 aac 600
DB 4810 aac 4869
QY 601 accatgctgggaagagagaggtggtcacaagtcacaggaactaagcccttggccacag 660
DB 4870 accatgctgggaagagagaggtggtcacaagtcacaggaactaagcccttggccacag 4929
QY 661 cccac 719
DB 4930 cccac 4989
QY 720 atcatctctgtctgagcagtgagaggtggtgtaagtcacagaagaatggttcgaagtcagaa 779
DB 4990 atcatctctgtctgagcagtgagaggtggtgtaagtcacagaagaatggttcgaagtcagaa 5049
QY 780 gatataagaataagtgagtgatgtaacacacacacacacacacacacacacacacac 839
DB 5050 gatataagaataagtgagtgatgtaacacacacacacacacacacacacacacacac 5109
QY 840 ccagaatgctgctcattccacatgaanaagtgctcatacacatgagaaacacacacacac 899
DB 5110 ccagaatgctgctcattccacatgaanaagtgctcatacacatgagaaacacacacacac 5169
QY 900 acaaaagtgcatataatgcaattatlttaataaagaatacattatataattctt 959

DB 5170 acaaaagtgcatataatgcaattatlttaataaagaatacattatataattctt 5229
QY 960 atagaanaaagctcgggaagagtttacttcaattgttagcaatgctcaggtggcgagatc 1019
DB 5230 atagaanaaagctcgggaagagtttacttcaattgttagcaatgctcaggtggcgatc 5289
QY 1020 aggtgatttcttcttaactcgttaatttcaatgtaattcttcttcaatttcttcaatgaa 1079
DB 5290 aggtgatttcttcttcaactcgttaatttcaatgtaattcttcttcaatttcttcaatgaa 5349
QY 1080 gatgaattcctgtatataaataaagaanaaataatcttgaggttaagcagagacaa 1139
DB 5350 gatgaattcctgtatataaataaagaanaaataatcttgaggttaagcagagacaa 5409
QY 1140 tcatctctgattgtctcagac 1199
DB 5410 tcatctctgattgtctcagac 5469
QY 1200 tgcctcctcgtctgtttagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1259
DB 5470 tgcctcctcgtctgtttagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 5529
QY 1260 ggaagctgctgctgagcttctgctgctgagacacacacacacacacacacacacacac 1319
DB 5530 ggaagctgctgctgagcttctgctgctgagacacacacacacacacacacacacacac 5589
QY 1320 tcatctctgatttcttcttcaagaagatcacagcccttgaggttccaaagcttgatcc 1379
DB 5590 tcatctctgatttcttcttcaagaagatcacagcccttgaggttccaaagcttgatcc 5649
QY 1380 agcttcaagaagcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1439
DB 5650 agcttcaagaagcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5709
QY 1440 tggaaatcagctcgtgagtttaattgaggaataagctcctcgcagatgagtttaag 1499
DB 5710 tggaaatcagctcgtgagtttaattgaggaataagctcctcgcagatgagtttaag 5769
QY 1500 acaaaagtgcatataatgcaattatlttaataaagaatacattatataattctt 1559
DB 5770 acaaaagtgcatataatgcaattatlttaataaagaatacattatataattctt 5829
QY 1560 aaggaagagacacagagacagagagacgcgggaagacatacgtlaaaga tgaagcagag 1619
DB 5830 aaggaagagacacagagacagagagacgcgggaagacatacgtlaaaga tgaagcagag 5889
QY 1620 atcggagttctgcaagccacaagctlaagaaacacacacacacacacacacacacacac 1679
DB 5890 atcggagttctgcaagccacaagctlaagaaacacacacacacacacacacacacacac 5949
QY 1680 tggagaagtcagaagaataatcttccctagaagctttagaggaataacgctctgtgaa 1739
DB 5950 tggagaagtcagaagaataatcttccctagaagctttagaggaataacgctctgtgaa 6009
QY 1740 accttaatcagacttccagcctccctcgaagcagaagaataaataatcttgcgtctttaa 1799
DB 6010 accttaatcagacttccagcctccctcgaagcagaagaataaataatcttgcgtctttaa 6069
QY 1800 gccaccaagataatgtgttacagacagctctaggaataataacagctgctaaatgatac 1859
DB 6070 gccaccaagataatgtgttacagacagctctaggaataataacagctgctaaatgatac 6129
QY 1860 cctgtctcctcgtgtttaaattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1919
DB 6130 cctgtctcctcgtgtttaaattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6189
QY 1920 tctgtaaccaatagatacagcagaagtgatgcatgacacacacacacacacacacacacacac 1979
DB 6190 tctgta -ccaaatagaatacagcagaagtgatgcatgacacacacacacacacacacacacacac 6248
QY 1980 aagaacatgacagcttctacttgagccctctcctctgcaacacacacacacacacacacacac 2039
DB 6249 aagaacatgacagcttctacttgagccctctcctctgcaacacacacacacacacacacacac 6308

Accession	Sequence	Position
OY 2040	ttgtctcaactcgcctcttggggggaagcctacgcttgcacatgcatactgtgacagccctataaagagac	20399
Db 6309	cttggtccactccgcctctggggggaagcctacgcttgcacatgcatactgtgacagccctataaagagac	6368
OY 2100	ttaacgttggtlaaaaaatgaaatgcctctctctgcacacagccacactatgctgaacctagaagcagag	2159
Db 6369	ttatcgttggtlaaaaaatgaaatgcctctctctgcacacagccacactatgctgaacctagaagcagag	6428
OY 2160	acctctggagataaactcagatcttctgtcttctaagtgtgcacagtttttggctcctaactgtta	2219
Db 6429	acctctggagataaactcagatcttctgtcttctaagtgtgcacagtttttggctcctaactgtta	6488
OY 2220	ttgcagcaatagataataataataatgcagaagaagag	2253
Db 6489	ttgcagcaatagataataataataatgcagaagaagag	6522

RESULT 4
AAZ30053 standard; DNA: 7605 BP.

LT	4
0053	
AAZ30053 standard; DNA; 7605 BP.	
AAZ30053;	
Query Match	96.8%; Score 2180.4; DB 20; Length 7605;
Best local similarity	99.1%; Pred. No. 0;
Matches 2234; Conservative	0; Mismatches 16; Indels 4; Gaps 4;

XX	26-JAN-2000	(first entry)
DT	DNA encoding a human interleukin-1 receptor antagonist.	
DE		
XX		
XX		
KW	Human: interleukin-1 receptor; IL-1; antagonist; sepsis;	
KW	acute pancreatitis; endotoxic shock; cytokine induced shock;	
KW	rheumatoid arthritis; chronic inflammatory arthritis;	
KW	pancreatic cell damage; diabetes mellitus type 1;	
KW	graft versus host disease; inflammatory bowel disease;	
KW	inflammation; pulmonary disease; autoimmune disease;	
KW	inflammatory disease; antiproliferative; myelogenous leukemia;	
KW	premature labor; intrauterine infection; nutritional activity;	
KW	hematopoiesis regulating activity; tissue growth activity;	
KW	activin activity; inhibit activity; chemotactic activity;	
KW	chemokinetic activity; hemostatic activity; thrombolytic activity;	
KW	anti-inflammatory activity; ss.	
XX		
XX		
OS	Homo sapiens.	
PN		
XX		
XX	MO9951744-A2.	
PD		
XX	14-OCT-1999.	
PD		
XX		
PE	05-APR-1999; 99WO-US04291.	
XX		
XX		
XX	03-APR-1998; 98US-0055010.	
XX	15-MAY-1998; 98US-0079909.	
XX	20-MAY-1998; 98US-0082264.	
PR	19-JUN-1998; 98US-0099818.	
PR	31-JUL-1998; 98US-0127698.	
PR	13-JAN-1999; 99US-0229591.	
PR	17-FEB-1999; 99US-0251370.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;	
PI	Leshkowitz D, Kita D, Ford J, Pace A, Alfento M;	
XX		
DR	WPI; 1999-611042/52.	
XX		
XX		
PT	New isolated interleukin-1 receptor binding polypeptides, used to treat	
PT	e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,	
PT	inflammatory disease, autoimmune disease or proliferative disease	
XX		
PS	Disclosure; Fig 10A-C; 123pp; English.	
CC	The present sequence encodes a human interleukin-1 (IL-1) receptor	
CC	antagonist. It is an extension of AA230052. The encoded polypeptide is	
CC	capable of binding IL-1 receptors (IL-1Rs). The polynucleotides and	

polypeptides can be used for the prevention or treatment of disorders involving sepsis, acute pancreatitis, endotoxic shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections. They can also exhibit activities such as e.g. nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity receptor/ligand activity, and anti-inflammatory activity. The products can also be used for detection, diagnosis and drug screening.

Query Match	96.8%	Score 2180.4	DB 20	Length 7605
Best Local Similarity	99.1%	Pred. No. 0		
Matches 2234	Conservative	0	Mismatches 16	Indels 4
				Gaps 4
OY 1	aatccagaagcttcacactctctacccgagcgagaaatctgggtctacactccagcttcgagtcgg	60		
Db 5144	aatccagaagcttcacactctctacccgagcgagaaatctgggtctacactccagcttcgagtcgg	5203		
OY 61	ctgcctaccgggctcgtctccctcgtcgaacgtctcctgaagccgcatcagccgtctcagatca	120		
Db 5204	ctgcctaccgggctcgtctccctcgtcgaacgtctcctgaagccgcatcagccgtctcagatca	5263		
OY 121	cccaagcttcccgagaatctgtctgagatgcccacatcaagactcttactctccagcagt	180		
Db 5264	cccaagcttcccgagaatctgtctgagatgcccacatcaagactcttactctccagcagt	5323		
OY 181	gtgactgagggcaacgtctgccccccagaaactccctctggagagagccagctctgggtctga	240		
Db 5324	gtgactgagggcaacgtctgccccccagaaactccctctggagagagccagctctgggtctga	5382		
OY 241	gagctgagagagaccatctgctcgagacaatactactcttctctctctccagagaccacagctga	300		
Db 5383	gagctgagagagaccatctgctcgagacaatactactctctctctctccagagaccacagctga	5442		
OY 301	cttagctgggacactctgacacactctgtctctctgtctcccaagtttcgataaattctgagatt	360		
Db 5443	cttagctgggacactctgacacactctgtctctctgtctcccaagtttcgataaattctgagatt	5502		
OY 361	ggagcttaagctccaggggtctctcccccactctgagatggtctgacacgtctggaacctctgtaaaa	420		
Db 5503	ggagcttaagctccaggggtctctcccccactctgagatggtctgacacgtctggaacctctgtaaaa	5562		
OY 421	accctctggggtctaaactctgagaaataacatgaaaaagtctctctgctggggctggggctggag	480		
Db 5563	accctctggggtctaaactctgagaaataacatgaaaaagtctctctgctggggctggggctggag	5622		
OY 481	tgctcgggaatcatctccctgcttaattggttaactctgacaagtctgtacccctgagcccgagacc	540		
Db 5623	tgctcgggaatcatctccctgcttaattggttaactctgacaagtctgtacccctgagcccgagacc	5682		
OY 541	aaaccatcccccagcttgagcccttataggtctagctgctctccacatgaaagctccctcctaac	600		
Db 5683	aaaccatcccccagcttgagcccttataggtctagctgctctccacatgaaagctccctcctaac	5742		
OY 601	accactctgacagagagaggggtctgtctcatagagctcaggaatctatctgacctctggcccaag	660		
Db 5743	accactctgacagagagaggggtctgtctcatagagctcaggaatctatctgacctctggcccaag	5802		
OY 661	ccacccccctctccctctt-attcctcgaactgcatatgtctactcttccatcttccctcc	719		
Db 5803	ccacccccctctccctcttactctctgcaactctgcatatgtctactcttccatcttccctcc	5862		
OY 720	atcatctctgtctgtgagcatctgagagagctgtgtgagcttcagagaanaatgtctcagctcagaa	779		

Db 6043 acaaagtgcataatgtcaattttaaataaagatacctatttatatttctt 6102

Db 7121 aagacactgcagcttctacttgagccctctctctctgccaaccaacgcccccaatctatc 7180

QY 2040 ttgctcactcgtctcgtggaagctagctcgtcgtatgacgaagccataaagac 2099
|||||
Db 7181 ttggccactcgtcgtcgtggaagctagctcgtcgtatgacgaagccataaagac 7240
QY 2100 ttacgttgtaaaaaatgaagctcctcgtccacagacacatlaagtgaactagaagcagag 2159
|||||
Db 7241 ttatggttaaaaaatgaagctcctcgtccacagacacatlaagtgaactagaagcagag 7300
QY 2160 acctctgtgagataatcgaagtgtgtgttttaagtgtcctcaagtttgggttaactgtta 2219
|||||
Db 7301 acctctgtgagataatcgaagtgtgtgttttaagtgtcctcaagtttgggttaactgtta 7360
QY 2220 ttgacgaatagataataatcatcagagaaagag 2253
|||||
Db 7361 ttgacgaatagataataatcatcagagaaagag 7394

RESULT 6
1354
AAF31354 standard: cDNA; 2647 BP.

AC AAF31354;
XX
DT 05-APR-2001 (first entry)
XX
DE Extension of B2HFLS20W cDNA library sequence #2.
XX
KM Interleukin: IL-1 receptor; cancer: Inflammation; ss.
XX
OS Homo sapiens.
XX
PN MO200102571-A2.
XX
PD 11-JAN-2001.
XX
PF 07-JUL-2000; 2000MO-US18710.
XX
PR 07-JUL-1999; 99US-0348942.
PR 13-OCT-1998; 98US-0417455.
PR 08-DEC-1999; 99US-0457626.
PR 10-MAR-2000; 2000US-0523552.
PR 22-MAY-2000; 2000US-0576008.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Pace A;
WPI: 2001-071582/08.

PT Isolated nucleic acids encoding interleukin-1 (IL-1) receptor
PT antagonist proteins (referred as IL-1hY1), useful in the treatment of
PT cancer, e.g. breast adenocarcinoma and brain tumors, and an
PT inflammatory disease mediated by IL-18 -
XX
XX
PS Claim 1; Fig 8; 179pp; English.
XX
XX
CC The present invention relates to interleukin (IL)-1 receptor
CC antagonist proteins. IL-1hY1 is useful for treating cancer,
CC an inflammatory disease mediated by IL-18, inflammation
CC resulting from infection or allergic reactions, and inflammation
CC associated with chronic bronchitis, arthritis, diabetes or
CC endothermia.
XX
XX
SQ Sequence 2647 BP; 743 A; 589 C; 644 G; 671 T; 0 other;

Query Match 96.7%; Score 2178.4; DB 22; Length 2647;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2240; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 1 aatccaagagcttacccttaccgagcggaatggggtcaccctcaggtcgaatcg 60
|||||
Db 342 aatccaagagcttacccttaccgagcggaatggggtcaccctcaggtcgaatcg 401

QY 61 ctgcttaccgggcttggttctctgtgacagggtgacctgaagccgaatcagccctgtcagactca 120
|||||
Db 402 ctgcttaccgggcttggttctctgtgacagggtgacctgaagccgaatcagccctgtcagactca 461
QY 121 ccagacttcccgagaaatggtgtgctggaatgcccccatcacaagacttctacttccagcagt 180
|||||
Db 462 ccagacttcccgagaaatggtgtgctggaatgcccccatcacaagacttctacttccagcagt 521
QY 181 gtgactagggcaacgttgcctcccccagaactcccttgggcagagcagctcgggtgaggggt 240
|||||
Db 522 gtgactagggcaacgttgcctcccccagaactcccttgggcagagcagctcgggtgaggggt 580
QY 241 gaatgagaggagaccatctggtgagacaaatcaactcttctgctcctaaggagccccgggtctga 300
|||||
Db 581 gaatgagaggagaccatctggtgagacaaatcaactcttctgctcctaaggagccccgggtctga 640
QY 301 cttagtgggacccctggaacacattgtctctgtgtccagtttgataaaatctcgaagattc 360
|||||
Db 641 cttagtgggacccctggaacacattgtctctgtgtccagtttgataaaatctcgaagattc 700
QY 361 ggaagctcgaatccagaggtcctcccccacctggaatggtgctactgctgtggaacctgtgaaaa 420
|||||
Db 701 ggaagctcgaatccagaggtcctcccccacctggaatggtgctactgctgtggaacctgtgaaaa 760
QY 421 accatgtgggttaaacctgggaataacatgaaagaattctcgtgggggtgggggtgggggag 480
|||||
Db 761 accatgtgggttaaacctgggaataacatgaaagaattctcgtgggggtgggggtgggggag 820
QY 481 ttgctgggaatcattctcctgtccttaattgttaacttgacaagtgttacccctgagcccgagcc 540
|||||
Db 821 ttgctgggaatcattctcctgtccttaattgttaacttgacaagtgttacccctgagcccgagcc 880
QY 541 aacccttcccccagttgagcccttaaggttgagtgagtgagcttcacatgaaagtccctcactc 600
|||||
Db 881 aacccttcccccagttgagcccttaaggttgagtgagtgagcttcacatgaaagtccctcactc 940
QY 601 accacgtgtgagagagaggggtggtgcatatgaatcagaggtctatgtgacctgtggccagc 660
|||||
Db 941 accacgtgtgagagagaggggtggtgcatatgaatcagaggtctatgtgacctgtggccagc 1000
QY 661 cccaccccttccctctt-accctgacactgtcattatgtctacaccttccctaccttccctc 719
|||||
Db 1001 cccaccccttccctctt-accctgacactgtcattatgtctacaccttccctaccttccctc 1060
QY 720 atcatctgtgtgtggcattgagaggtgtgtgattgctcagaagaatgggttcgagctcaga 779
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Db 1061 atcatctgtgtgtggcattgagaggtgtgtgattgctcagaagaatgggttcgagctcaga 1120
QY 780 gatataaagataagtaggtatgtgtgactcctctttaaaccaccaaagataacataaattc 839
|||||
Db 1121 gatataaagataagtaggtatgtgtgactcctctttaaaccaccaaagataacataaattc 1180
QY 840 ccagatgtgtgtctctatctcccatgaaaaagtgtctcagacatctgagaagaactactc 899
|||||
Db 1181 ccagatgtgtgtctctatctcccatgaaaaagtgtctcagacatctgagaagaactactc 1240
QY 900 acaaaagtggcatata-ttgcatttatttaattaaagaatcattatattatcttct 958
|||||
Db 1241 acaaaagtggcatataatttgcatttatttaattaaagaatcattatattatcttct 1300
QY 959 tatagaaaaaagctcgtgaagaagtttaactcaatgtgagaatgtcgaagggtggggcagta 1018
|||||
Db 1301 tatagaaaaaagctcgtgaagaagtttaactcaatgtgagaatgtcgaagggtggggcagta 1360
QY 1019 taagtgaatttcttcttaattctgttaattatctatctgtattctcctaatttctcacaatga 1078
|||||
Db 1361 taagtgaatttcttcttaattctgttaattatctatctgtattctcctaatttctcacaatga 1420
QY 1079 agatgaattctctgtataaaaaataagaagaataatcattctgaggttaagcagaagac 1138
|||||
Db 1421 agatgaattctctgtataaaaaataagaagaataatcattctgaggttaagcagaagac 1480

OY	1139	atctctctatctgtccctcaagcctcccaatctccccaagataaattcaaatcttaactgacct	1198
Db	1461	atcaatctctgatactgtctctcaagcctccaattccccaagataaattcaaatctgaactgacct	1540
OY	1199	ctctgctctctgttctgttctgttagttagtcatctcaagaaacagatctctcagacaagccactgagc	1258
Db	1541	ctctgctctctgtctgtgtctgttagttagtcatctcaagaaacagatctctcagacaagccactgagc	1600
OY	1259	agagagctgtgtgctgagagtttgttgtgctcttgaaatctctcggttaagagaaacttaagaaacaaa	1318
Db	1601	agagagctgtgtgctgagaaattctgtgtgctcttgaaatctctcggttaagagaaacttaagaaacaaa	1600
OY	1319	atcaatctctgataatctctctccataagagatcacacagcccccggagatcccaagcatctgtgact	1378
Db	1661	atcaatctctgataatctctctccataagagatcacagcccccggagatcccaagcatctgtgact	1720
OY	1379	cagctctctaagaagagctgtctgtactcgtgttgaaattgtgtctccctccaataatcaacatctctc	1438
Db	1721	cagctctctaagaagagctgtctgtactcgtgttgaaattgtgtctccctccaataatcaacatctctc	1780
OY	1439	cttgaaatctctcaagctctgtgaattctattcttgagataaagagctctctcgagatctgttagttaa	1498
Db	1781	cttgaaatctctcaagctctgtgaattctattcttgagataaagagctctctcgagatctgttagttaa	1840
OY	1499	gacaaagctcatctgtgatactgaaggtagaacctaaattcaatatagactgtgttccctgttata	1558
Db	1841	gacaaagctcatctgtgatactgaaggtagaacctaaattcaatatagactgtgttccctgttata	1900
OY	1559	aaagagagagagacaaagagagagagagagagcggggagagagctctgtataagatctgaagcgaga	1618
Db	1901	aaagagagagagacaaagagagagagagagagcggggagagagctctgtataagatctgaagcgaga	1960
OY	1619	gactcgagcttcttgacgaccaaagcttaagaaacaccaaagagattgtgtgcacaacatcagaagc	1678
Db	1961	gactcgagcttcttgacgaccaaagcttaagaaacaccaaagagattgtgtgcacaacatcagaagc	2020
OY	1679	cttgaaagagagcgaagagaagaaattcttccctcagaagagctcttgaaagagataacgctctgctgca	1738
Db	2021	cttgaaagagagcgaagagaagaaattcttccctcagaagagctcttgaaagagataacgctctgctgca	2080
OY	1739	aaccttaatctcagagacttccagcctctctgaacagaaagaaagataaattctgcgctgttta	1798
Db	2081	aaccttaatctcagagacttccagcctctctgaacagaaagaaagataaattctgcgctgttta	2140
OY	1799	agccacaagaagataaattctgtgttaacagagctctctagagaaactataacagctgtctaaagatgac	1858
Db	2141	agccacaagaagataaattctgtgttaacagagctctctagagaaactataacagctgtctaaagatgac	2200
OY	1859	ccctgctctccctggtgttaacatctgt	1918
Db	2201	ccctgctctccctggtgttaacatctgt	2260
OY	1919	cttgttgacccaataagaaatctgacagagaagtgtatgtgtgcactctccaaagtattagtata	1978
Db	2261	cttgttgacccaataagaaatctgacagagaagtgtatgtgtgcactctccaaagtattagtata	2319
OY	1979	aaaaaagcgtcagctcttactatttgaaagccctctctctctgacacccacccgcccccaatctat	2038
Db	2320	aaaaaagcgtcagctcttactatttgaaagccctctctctctgacacccacccgcccccaatctat	2379
OY	2039	cttgtgcacaaatctgctctctgt	2098
Db	2380	cttgtgcacaaatctgctctctgt	2439
OY	2099	cttaacgtgtgtataaaaaatgtgaagctctctgtccacagccacacattagtgtgaacctagaagcaga	2158
Db	2440	cttaacgtgtgtataaaaaatgtgaagctctctgtccacagccacacattagtgtgaacctagaagcaga	2499
OY	2159	gacccctgttgagataaactgataagttgt	2217
Db	2500	gacccctgtgtgagataaactgataagttgt	2559
OY	2218	tatgcagcaaatagataaataataatctgcagagaaagc	2253

Db 2560 tatgcagcaatagataataataatgcagagaaagag 2595

RESULT 7

ID AAZ30051 standard; cDNA; 2648 BP.

AC AAZ30051;

DT 26-JAN-2000 (first entry)

DE cDNA encoding a human interleukin-1 receptor antagonist

Human; interleukin-1 receptor; IL-1; antagonist; sepsis;

KW rheumatoid arthritis; chronic inflammatory arthritis;

KW graft versus host disease; inflammatory bowel disease

inflammatory disease; antiproliferative; myelogenous leukemia; KW

hematopoiesis regulating activity; tissue growth activity;

KW chemokinetic activity; hemostatic activity; thrombolytic activity;

XX
2

XX
DN 100051744-23

XX 14-0000-1000
BD

XX 05-APR-1999. 0000-11504291
DE

XX	03-APR-1998	98RUC-0055010
DP		

PR	15-MAY-1998;	98US-0079909.
PR	20-MAY-1998;	98US-0082364

PR	19-JUN-1998;	9805-0099818.
PR	31-JUL-1998:	9805-0127698

PR	13-JAN-1999;	99US-0229591.
PR	17-FEB-1999;	99US-0251370

XX
PA (HYSE-) HYSEO INC.

Drmanac R., Crkventjakov R., Dickson M., Drmanac S., Tabat T.;
XX
PI

PI Lesnkowitz D, Kita D, Ford J, Pace A, Altenito M,
XX

DR WPI; 1999-611042/52.
XX

PT New isolated interleukin-1 receptor binding polypeptides, used to treat

PT inflammatory disease, autoimmune disease or proliferative disease - XX

PS Claim 1; Fig 8; 123pp; English.

CC The present sequence encodes a human Interleukin-1 (IL-1) receptor
CC antagonist. It is an extension of AAZ30050. The encoded polypeptide

capable of binding IL-1 receptors (IL-1Rs). The polynucleotides and polynucleotides can be used for the prevention or treatment of disorders

CC shock: rheumatoid arthritis, chronic inflammatory arthritis, pancreatitis

CC cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary CC

CC disease, other autoimmune disease or inflammatory disease, an
CC antiproliferative agent such as for acute or chronic myelogenous

leukemia or in the prevention of premature labor secondary to intrauterine infections. They can also exhibit activities such as a

CC - nutritional activity, cytokine and cell proliferation/differentiation
CC - activity: immune stimulating or suppressing activity: hematopoiesis

CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, regulating activity, tissue growth activity, activin/inhibin activity, CC

CC receptor/ligand activity, and anti-inflammatory activity. The product

CC can also be used for detection, diagnosis and drug screening.
XX
Sequence 2648 BP; 744 A; 589 C; 644 G; 671 T; 0 other;

Query Match 96.7%; Score 2178.4; DB 20; Length 2648;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2240; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

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QY 61 cgcgcacacgggctggtctcctctgacaggtctcgaagcccatcagctctgacatca 120
DB 402 cgcgcacacgggctggtctcctctgacaggtctcgaagcccatcagctctgacatca 461
QY 121 ccagagctccgagaaatggctggatggcccccatcacaagacttacttccagagtc 180
DB 462 ccagagctccgagaaatggctggatggcccccatcacaagacttacttccagagtc 521
QY 181 gtagctaggagcaactgtccccccagaactccctgggcagagccagctcggttgaggt 240
DB 522 gtagctaggagcaactgtccccccagaactccctgggcagagccagctcggttgaggt 580
QY 241 ggttgaggagagcccatggcgcgacaaatcaactctctctctcagagaccggctcga 300
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QY 301 cttaagtggagacctgacacctctgtctctggcttcccaagtctgacaaatcttgagatct 360
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DB 1841 gacaagctcagctgt 1900
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DB 2081 aaccttaatctcagacttccagcctcccgaaacgaagaataaaattcgcgctgttca 2140
QY 1799 agccacaaaggaataattgtttacagagctctaggaactataagcgtctaaagtat 1858
DB 2141 agccacaaaggaataattgtttacagagctctaggaactataagcgtctaaagtat 2200
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DB 2261 ttctgtacccaaatagaataatggcagaagtgtatgtcacttccaaagttaggttata 2319
QY 1979 aaaagacatgcagctctctactgtagcctctctctgtccacccaacgcccccaactat 2038
DB 2320 aaaagacatgcagctctctactgtagcctctctctgtccacccaacgcccccaactat 2379
QY 2039 ctgtgtcactcgtctcgtggggaagctagctgcacatgtatgacgacctataagaaga 2098

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Db 2380 ctggcgcaactcgtctgggggaagtaagctgacatgcatgagcagcctataaagaga 2439
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Db 2500 gactcgtgagataacgcattgttctgttctttaaagttgctcagttctgtcctaactgt 2559
Qy 2218 tatcgagcaatagataaataatgacagagaagag 2253
Db 2560 tatcgagcaatagataaataatgacagagaagag 2595

RESULT 8
AAZ50813
ID AAZ50813 standard; cDNA; 2490 BP.
XX
AC AAZ50813;
31-MAY-2000 (first entry)

Human TANGO-93 cDNA with additional 3'UTR sequence.
DE
XX TANGO-93; cytokine; human; secreted protein; IL-1 expression; cancer;
XX Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
XX immunosuppressive; antihemematic; antiarthritic; antipsoriatic; asthma;
XX antiinflammatory; antibacterial; antitumor; cyostatic; immunomodulator;
XX osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
XX graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;
XX septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
XX liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
XX autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
XX systemic lupus erythematosus; forensic; transgenic animal; SS.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 63..530
XX /tag=a
XX /product="Human TANGO-93 protein"
XX /note="Has 53% homology to human Interleukin-1 receptor
XX 3'UTR 531..2490
XX /tag=b
XX /note="Additional sequences"

XX MO200008045-A2.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99MO-US17886.
XX
XX 07-AUG-1998; 98US-0131263.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Pan Y;
XX
XX MPI; 2000-205669/18.
XX
XX Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful
XX for treating a variety of cellular processes e.g. asthma, rheumatoid
XX arthritis, psoriasis and autoimmune diseases
XX
XX Example 2; Fig 5; 113pp; English.
XX
XX The present sequence is the cDNA encoding the human TANGO-93, with
XX additional 3'UTR sequence. It is a secreted protein that belongs to the
XX cytokine superfamily. It plays a role similar to secreted interleukin-1
XX receptor antagonist (IL-1ra). TANGO-93 modulates immune mediated
```

```
CC inflammation and IL-1 gene or protein expression. TANGO-93 is useful as
CC a modulating agent for regulating cellular processes like asthma, graft
CC vs-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel
CC disease, septic shock, ulcerative colitis, Crohn's disease, chronic
CC myelogenous leukemia, cancer, liver disease, and autoimmune diseases,
CC osteoarthritis, Lyme disease, cachexia, and Crohn's disease, e.g.
CC myasthenia gravis, autoimmune diabetes and systemic lupus erythematosus.
CC Partial TANGO-93 sequences are useful in forensic biology, for diagnostic
CC and prognostic assays, prophylactic and therapeutic treatment and
CC pharmacogenomics. The DNA sequences are useful as hybridization probes
CC and primers, for isolation of TANGO-93 sequence and for the creation of
CC transgenic animals.
XX
XX SQ Sequence 2490 BP; 650 A; 571 C; 619 G; 650 T; 0 other;
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Query Match 89.7%; Score 2020.6; DB 21; Length 2490;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2138; Conservative 0; Mismatches 9; Indels 72; Gaps 4;
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Qy 61 ctgctaccgggctggtctcctgacagtgctgaaagccgatcagctcagactca 120
Db 403 ctgctaccgggctggtctcctgacagtgctgaaagccgatcagctcagactca 462
Qy 121 ccaggtcccgagaatggtgctggaatgcccatcagaagcttactcagaagct 180
Db 463 ccaggtcccgagaatggtgctggaatgcccatcagaagcttactcagaagct 522
Qy 181 gtacacaggagcaacgtgccccccagaaactccctgagagagcagactcgggtga 240
Db 523 gtacacaggagcaacgtgccccccagaaactccctgagagagcagactcgggtga 581
Qy 241 gaatgagagagaccatgaggacaatcaactcttctgcttcagagaccacagctga 300
Db 582 gaatgagagagaccatgaggacaatcaactcttctgcttcagagaccacagctga 641
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Db 642 cttagtgggacactgacacttctgtcttcttccaggttgataaatctgaagtt 701
Qy 361 ggaagctcaatccagggtccctcccccacatgagtgctactgctgtaaacctgt 420
Db 702 ggaagctcaatccagggtccctcccccacatgagtgctactgctgtaaacctgt 761
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Db 882 aaccctacccagcttgagctctatagggctcagtgacttcacatgaaagctctc 941
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Db 942 accacgtgcaagagagaggtggtcatatagatcagaagatctatgcccctggccagc 1001
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Qy 780 gataaagaataagtaggtatgctatcctctttaaataaccacaagatacaataa 839
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Db 5430 atcaatcgtgaattcttctcctaagaagatcacagcccttgagatcccaagcattgac 5489
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 Db 5490 caatctctaagaagctgctgctgactggtgaattgtgtcccccctaattacatcttc 5549
 Qy 1439 ttggaatctcaagctgtgagttatttggagataagagctctgcagatgtagttaa 1498
 Db 5550 ttggaatctcaagctgtgagttatttggagataagagctctgcagatgtagttaa 5609
 Qy 1499 gacaagatctgctgagatgaagatgacttaataatcatatgactggtcttctgtatga 1558
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 Qy 1559 aagagagagacacagacagagagagacgcgcgggaagactatgtaagaatgaagcaga 1618
 Db 5670 aagagagagacacagacagagagagacgcgcgggaagactatgtaagaatgaagcaga 5729
 Qy 1619 gacggagatttgacagcaca 1640
 Db 5730 gacggagatttgacagcaca 5751
 RESULT 11
 AA230052
 ID AA230052 standard; DNA; 5752 BP.
 AC AA230052:
 XX
 DT 26-JAN-2000 (first entry)
 DE
 XX
 DE DNA encoding a human interleukin-1 receptor antagonist.
 XX
 KW Human: interleukin-1 receptor; IL-1; antagonist; sepsis;
 KW acute pancreatitis; endotoxin shock; cytokine induced shock;
 KW rheumatoid arthritis; chronic inflammatory arthritis;
 KW graft versus host disease; diabetes mellitus type 1;
 KW inflammation; pulmonary disease; autoimmune disease;
 KW inflammatory disease; antiproliferative; myelogenous leukemia;
 KW premature labor; intrauterine infection; nutritional activity;
 KW hematopoiesis regulating activity; tissue growth activity;
 KW activin activity; inhibin activity; chemotactic activity;
 KW chemokinetic activity; hemostatic activity; thrombolytic activity;
 KW anti-inflammatory activity; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9951744-A2.
 XX
 F 14-OCT-1999.
 XX
 PF 05-APR-1999; 99WO-US04291.
 XX
 XX 03-APR-1998; 98US-0055010.
 PR 15-MAY-1998; 98US-0079909.
 PR 20-MAY-1998; 98US-0082364.
 PR 19-JUN-1998; 98US-0099818.
 PR 31-JUL-1998; 98US-0127698.
 PR 13-JAN-1999; 99US-0229591.
 PR 17-FEB-1999; 99US-0251370.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Ford J, Pace A, Alfemio M;
 XX
 DR WPI; 1999-611042/52.
 XX
 PT New isolated interleukin-1 receptor binding polypeptides, used to treat
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
 PT inflammatory disease, autoimmune disease or proliferative disease
 XX

PS Claim 1; Fig 9A-C; 123pp; English.
 XX
 CC The present sequence encodes a human interleukin-1 (IL-1) receptor
 CC antagonist. It represents the genomic sequence of AA230046-51. The
 CC encoded polypeptide is capable of binding IL-1 receptors (IL-1Rs). The
 CC polynucleotides and polypeptides can be used for the prevention or
 CC treatment of disorders involving sepsis, acute pancreatitis, endotoxin
 CC shock, cytokine induced shock, rheumatoid arthritis, chronic
 CC inflammatory arthritis, pancreatic cell damage from diabetes mellitus
 CC type 1, graft versus host disease, inflammatory bowel disease,
 CC inflammation associated with pulmonary disease, other autoimmune disease
 CC or inflammatory disease, an antiproliferative agent such as for acute or
 CC chronic myelogenous leukemia or in the prevention of premature labor
 CC secondary to intrauterine infections. They can also exhibit activities
 CC such as e.g. nutritional activity, cytokine and cell proliferation/
 CC differentiation activity, immune stimulating or suppressing activity,
 CC hematopoiesis regulating activity, tissue growth activity, activin/
 CC inhibin activity, chemotactic/chemokinetic activity, hemostatic and
 CC thrombolytic activity, receptor/ligand activity, and anti-inflammatory
 CC activity. The products can also be used for detection, diagnosis and
 CC drug screening.
 CC
 XX
 SQ Sequence 5752 BP; 1467 A; 1274 C; 1489 G; 1383 T; 139 other;
 Query Match 69.5%; Score 1566.6; DB 20; Length 5752;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1624; Conservative 5; Mismatches 9; Indels 5; Gaps 5;
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Oy	780	gataaaagaataaagttaaggtgtatgtctgtactctctttaaaaaaccaagatacaaatcaaat-	838
Db	4891	gataaaagaataaagttaaggtgtatgtctgtactctctttaaaaaaccaagatacaaatcaaat-	4950
Oy	839	cccgagatgcgtgtctctcatctcccaatgaaaaagtggtccatgacatatgtgaagaacctact	898
Db	4951	cccgagatgcgtgtctctcatctcccaatgaaaaagtggtccatgacatatgtgaagaacctact	5010
Oy	899	tacaaagtgtgcataataatgtcaaatlttatcttaaatlaaagaatacctatatataatlttct	958
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RESULT	12
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ID	AAZ50812 standard; cDNA; 1323 BP.
XX	

XX	AAZ50812;	
XX	31-MAY-2000 (first entry)	
DT		
XX		
DE	Human TANGO-93 cDNA.	
XX		
XX	TANGO-93; cytokine; human; secreted protein; IL-1 expression; cancer;	
KW	Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiproliferative;	
KW	immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; forensic;	
KW	antiinflammatory; antibacterial; antitumor; cytostatic; immunomodulator;	
KW	osteopethtic; dermatological; antidiabetic; psoriasis; ulcerative colitis;	
KW	graft vs host disease; rheumatoid arthritis; inflammatory bowel disease;	
KW	septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;	
KW	liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;	
KW	autoimmune disease; myasthenia gravis; pharmacogenomic; chromosome 2;	
KW	diagnosis; asthma; systemic lupus erythematosus; transgenic animal; ss.	
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OS	Homo sapiens.	
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FH	Key	Location/Qualifiers
FT	CDS	57..524
FT		/tag= a
FT		/product= "Human TANGO-93 protein"
FT		/note= "Has 53% homology to human Interleukin-1 receptor
FT		antagonist (IL-1ra)"
FT		525..1323
FT	3'UTR	/tag= b
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PN	MO200008045-A2.	
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PD	17-FEB-2000.	
XX		
PF	06-AUG-1999;	99WO-US17886.
XX		
PR	07-AUG-1998;	98US-0131263.
XX		
PA	(MILL-) MILENNIUM BIOTHERAPEUTICS INC.	
XX		
PI	Pan Y;	
DR	WPI: 2000-205669/18.	
P-PSDB: AAY45062.		
XX		
PT	Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful	
PT	for treating a variety of cellular processes e.g. asthma, rheumatoid	
PT	arthritis, psoriasis and autoimmune diseases	
XX		
PS	Claim 2a; Fig 2; 113pp; English.	
XX		
CC	The present sequence is the cDNA encoding the human TANGO-93, a	
CC	secreted protein that belongs to the cytokine superfamily. It plays a	
CC	role similar to the secreted interleukin-1 receptor antagonist (IL-1ra)	
CC	and its expression is developmentally regulated in the uterus, placenta	
CC	and skeletal muscles. Human TANGO-93 gene is mapped to Chromosome 2,	
CC	within the IL-1 cluster. TANGO-93 modulates immune mediated inflammation	
CC	and IL-1 gene or protein expression. TANGO-93 is useful as a modulating	
CC	agent for regulating cellular processes like asthma, graft vs-host	
CC	disease, rheumatoid arthritis, psoriasis, inflammatory bowel disease,	
CC	septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous	
CC	leukaemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,	
CC	Lyme disease, cachexia, and autoimmune diseases e.g. myasthenia gravis,	
CC	autoimmune diabetes and systemic lupus erythematosus. Partial TANGO-93	
CC	sequences are useful in forensic biology, for diagnostic and prognostic	
CC	assays, prophylactic and therapeutic treatment and pharmacogenomics. The	
CC	DNA sequence is useful as hybridisation probe and primers, for isolation	
CC	of TANGO-93 sequence and for the creation of transgenic animals.	
XX		
Sequence 1323 BP; 315 A; 338 C; 353 G; 317 T; 0 other;		

Query Match	41.48;	Score 933.2;	DB 21;	Length 1323;
Best Local Similarity	99.08;	Pred. No. 8.4e-244;		
Matches 960;	Conservative 0;	Mismatches 8;	Indels 2;	Gaps 2;

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Db 397 ctgctaccgagctgttctctctgctgcaagctgctgcaagccgataagcctgtcaactca 456
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QY 840 ccaagatgctgctcctatcccatgaaagaatgctcatgacatcttgagaagaactcact 899
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RESULT 13
AAFP31352
ID AAFP31352 standard; cDNA; 985 BP.

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XX AC AAFP31352;
XX DT 05-APR-2001 (first entry)
XX DE B2HFLS20W cDNA library sequence #2.
XX KW Interleukin: IL-1 receptor; cancer; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200102571-A2.
XX PD 11-JAN-2001.
XX PF 07-JUL-2000; 2000MO-US18710.
XX PR 07-JUL-1999; 99US-0348942.
XX PR 13-OCT-1999; 99US-0417455.
XX PR 08-DEC-1999; 99US-0457626.
XX PR 10-MAR-2000; 2000US-0523552.
XX PR 22-MAY-2000; 2000US-0576008.
XX PA (HYSE-) HYSEQ INC.
XX PI Ford J, Pace A;
XX DR WPL; 2001-071582/08.
XX PT Isolated nucleic acids encoding Interleukin-1 (IL-1) receptor
XX PT antagonist proteins (referred as IL-1H1), useful in the treatment of
XX PT cancer, e.g. breast adenocarcinoma and brain tumors, and an
XX PT inflammatory disease mediated by IL-18 -
XX PS Claim 1; Fig 2; 179pp; English.
XX CC The present invention relates to Interleukin (IL)-1 receptor
XX CC antagonist proteins. IL-1H1 is useful for treating cancer,
XX CC an inflammatory disease mediated by IL-18, inflammation
XX CC resulting from infection or allergic reactions, and inflammation
XX CC associated with chronic bronchitis, arthritis, diabetes or
XX CC endohermia.
XX SQ Sequence 985 BP; 232 A; 264 C; 249 G; 240 T; 0 other;

Query Match 39.3%; Score 886.2; DB 22; Length 985;
Best Local Similarity 98.4%; Pred. NO. 4.5e-231;
Matches 916; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

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RESULT 14
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ID AAF31353 standard: cDNA: 1282 BP.

XX AAF31353:

05-APR-2001 (first entry)

XX Extension of B2HFLS20W cDNA library sequence #2.

KW Interleukin: IL-1 receptor; cancer; inflammation; ss.

XX Homo sapiens.

PN WO200102571-A2.

PD 11-JAN-2001.

PF 07-JUL-2000; 2000MO-US18710.

XX 07-JUL-1999; 99US-0348942.

PR 13-OCT-1999; 99US-0417455.

PR 08-DEC-1999; 99US-0457626.

PR 10-MAR-2000; 2000US-0523552.

PR 22-MAY-2000; 2000US-0576008.

XX (HYSE-) HYSEQ INC.

PI Ford J, Pace A;

XX MPI: 2001-071582/08.

```

XX Isolated nucleic acids encoding Interleukin-1 (IL-1) receptor
PT antagonist proteins (referred as IL-1Hv1), useful in the treatment of
PT cancer, e.g. breast adenocarcinoma and brain tumors, and an
PT inflammatory disease mediated by IL-18.
PS Claim 1; Fig 5; 179pp; English.
XX
CC The present invention relates to Interleukin (IL)-1 receptor
CC antagonist proteins. IL-1Hv1 is useful for treating cancer,
CC an inflammatory disease mediated by IL-18, inflammation
CC resulting from infection or allergic reactions, and inflammation
CC associated with chronic bronchitis, arthritis, diabetes or
CC endothermia.
XX
SQ Sequence 1282 BP; 294 A; 337 C; 350 G; 301 T; 0 other:

Query Match      39.3%; Score 886.2; DB 22; Length 1282;
Best Local Similarity 98.4%; Pred. No. 5.2e-231;
Matches 916; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

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Db 1012 ccacacccctccctt-attctgtcacatgataatgtaacctttctctctctcc 1071
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OY 720 atcatctgtgtgtgggcatgagaggtgtgtatgtcatagagaagtgtcgaagctcagaa 779
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Db 1072 atcatctgtgtgtgggcatgagaggtgtgtatgtcatagagaagtgtcgaagctcagaa 1131
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OY 780 gataaagataagtagaggatagtcgcgatccctctttaaaccgaagatacaatccaatc 839
 Db 1132 gataaaagataagtagaggatagtcgcgatccctctttaaaccgaagatacaatccaatc 1191
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 OY 900 acaaaagtgcatacatatgcgaattatttta 930
 Db 1252 acaaaagtgcatacatatgcgaattatttta 1282
 RESULT 15
 AAZ30050
 ID AAZ30050 standard; cDNA: 1282 BP.
 AC AAZ30050;
 XX
 PT 26-JAN-2000 (first entry)
 CDNA encoding a human interleukin-1 receptor antagonist.
 XX
 KW Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
 KW acute pancreatitis; endotoxin shock; cytokine induced shock;
 KW rheumatoid arthritis; chronic inflammatory arthritis;
 KW pancreatic cell damage; diabetes mellitus type 1;
 KW graft versus host disease; inflammatory bowel disease;
 KW inflammation; pulmonary disease; autoimmune disease;
 KW inflammatory disease; antiproliferative; myelogenous leukemia;
 KW premature labor; intrauterine infection; nutritional activity;
 KW hematopoiesis regulating activity; tissue growth activity;
 KW activin activity; inhibin activity; chemotactic activity;
 KW chemokine activity; hemostatic activity; thrombolytic activity;
 KW anti-inflammatory activity; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09951744-AZ.
 PD 14-OCT-1999.
 XX
 PF 05-APR-1999; 99MO-US04291.
 XX
 PR 03-APR-1998; 98US-0055010.
 PR 15-MAY-1998; 98US-0079909.
 PR 20-MAY-1998; 98US-0082364.
 PR 19-JUN-1998; 98US-0099818.
 PR 31-JUL-1998; 98US-0127698.
 PR 13-JAN-1999; 99US-0229591.
 PR 17-FEB-1999; 99US-0251370.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Ford J, Pace A, Allentio M;
 XX
 DR WPI: 1999-611042/52.
 DR P-PSDB: MAF43526.
 XX
 PT New isolated interleukin-1 receptor binding polypeptides, used to treat
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
 PT inflammatory disease, autoimmune disease or proliferative disease
 XX
 PS Claim 1; Flg 5; 123pp; English.
 XX
 CC The present sequence encodes a human interleukin-1 (IL-1) receptor
 CC antagonist. The encoded polypeptide is capable of binding IL-1
 CC receptors (IL-1Rs). The polynucleotides and polypeptides can be used for
 CC the prevention or treatment of disorders involving sepsis, acute
 CC pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid
 CC arthritis, chronic inflammatory arthritis, pancreatic cell damage from

	CC	diseases mellitus type 1, graft versus host disease, inflammatory bowel
	CC	disease, inflammation associated with pulmonary disease, other autoimmune
	CC	disease or inflammatory disease, an antiproliferative agent such as for
	CC	acute or chronic myelogenous leukemia or in the prevention of premature
	CC	labor secondary to intrauterine infections). They can also exhibit
	CC	activities such as e.g. nutritional activity, cytokine and cell
	CC	proliferation/differentiation activity, immune stimulating or
	CC	suppressing activity, hematopoiesis regulating activity, tissue growth
	CC	activity, activin/inhibin activity, chemotactic/chemokinetic activity,
	CC	hemostatic and thrombolytic activity, receptor/ligand activity, and
	CC	anti-inflammatory activity. The products can also be used for
	CC	detection, diagnosis and drug screening.
SQ	xx	
	Sequence 1282 BP; 293 A; 337 C; 350 G; 301 T; 1 other;	
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	Best Local Similarity	98.3%; Pred. No. 9,6e-231;
	Matches 915; Conservative	0; Mismatches 14; Indels 2; Gaps 2;
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QY	61	clygctaaccgggcttgtttccctgytagcaggltgccygaagccgatcaagcgltycagattca 120
Dd	413	ctygctaaccgggcttgtttccctgytagcaggltgccygaagccgatcaagcgltycagattca 472
QY	121	ccccagtctcccgagaatatgtgtgcttggatatygccccaaccaagactttactctcagcagct 180
Dd	473	ccccagtctcccgagaatatgtgtgcttggatatygccccaaccaagactttactctcagcagct 532
QY	181	gtgcacagaggaacaagcbycccccccaaacctccctggcgagagccacgctcgggtttaagggt 240
Dd	533	gtgcactaggggaagagtg - ccccccaaatccctcctggcgagagccacgctcgggttgagggt 591
QY	241	gagitggagagagaaccaatgycggaacaatcaactcttcctgccttcagagaccoccaaigtca 300
Dd	592	gagitggagagagaaccaatgycggaacaatcaactcttcctgccttcagagaccocceaigtca 651
QY	301	cttagtgggcacccctgacacacttgtcttcttggtttccagaittgcataatcttgagattt 360
Dd	652	cttagtgggcacccctgacacacttgtcttcttggtttccagaittgkataaatcttgagattt 711
QY	361	ggagctcaagtlccaaagytccctcccccaactggaatgtgtactatgctgtgtaaacttgtlaaa 420
Dd	712	ggagctcaagtlccaaagytccctcccccaactggaatgtgtactatgctgtgtaaacttgtlaaa 771
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Dd	892	aaaccaatcccaagttgagccttatbaagtgcagttagctctccaatgaaqtcctctcaactc 951
QY	601	acacactgtgcaggaggaaggaggtgtgcatalagagtaaggaatcatagagcccttggccagc 660
Dd	952	acacactgtgcaggaggaaggaggtgtgtcatalagagtaaggaatcatagagcccttggccagc 1011
QY	661	ccccaccccctccctt-atcctgcacatgtcatatgbtacccttccatactctccctc 719
Dd	1012	ccccaccccctccctt-aatcctgcacatgtcatatgbtacccttccatactctccctc 1071
QY	720	atacatctgtgtggagataaggaagtggtgtgtaatgcagaagaanaatgtgtgagtgtaagaa 779
Dd	1072	atacatctgtgtgtggagataaggaagtggtgtgtaatgcagaagaanaatgtgtgagtgtaagaa 1131
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Db 1132 gataaagaataagtaggtagtgcgtatcctctttaaaccacaagatatacaatcaaatc 1191
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Db 1192 ccagatgctgtctctatccatgaaaaagtgcctcatgacataattgagaagacctactt 1251
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Db 1252 ncaaaagtgcacataatctgcgaatttaattta 1282

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Search completed: March 1, 2002, 11:57:07
 Job time: 3267 sec

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3	643.2	28.5	697	11	BF509095	BF509095 UT-H-B14
4	527.8	23.4	555	10	AL138695	AL138695 UT-H-B14
5	465	20.6	467	13	AZ521126	AZ521126 RPT-11-1
6	451.2	20.0	485	10	A1040890	A1040890 owa26a12.x
7	435.8	19.3	464	11	BF435174	BF435174 nba343h02.1
8	426.8	18.9	464	10	A1813402	A1813402 w164a07.x
9	417	18.5	442	10	A1463847	A1463847 J188a08.x
10	413.8	18.4	726	11	B1089828	B1089828 602855071
11	404	17.9	922	10	AL545100	AL545100 AL545100
12	398.2	17.7	414	10	AA722902	AA722902 z981a03.s

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C	17	349.4	15.5	374	11	R70041
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C	19	315.4	14.0	348	11	R70089
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12-JUL-2001

RESULT	1		
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ACCESSION	BC000945		HITC
VERSION	BC000945		
KEYWORDS	BC000945.2	GI:14705316	
SOURCE	human.		

ORGANISM
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1648)

Author(s)	Title	Journal
Stussberg, A.	Direct Submission	National Institutes of Health, Mammalian
	Submitted (16-NOV-2000)	

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT	On Jul 12, 2001 this sequence version replaced g1:13937574.

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing center
Center code: BCM-HGSC

Web site: <http://www.ngsc.bcm.tmc.edu/cana/>
Contact: villalob@bcm.tmc.edu.

WILLIAMS, D.N., LUNA, R.A., HALE, S.M., HUIYK, S., LU, A., GARCIA A.M., HOLLOWAY, M., TELFORD, B., HODGSON, A., BOUCK, J., YU, W., MUZYNY, D.M., GIBBS, R.A.

Clone distribution: MGC clone distribution information can be found

driver population), a pool of clones from NCI-CGAP_Sub4 (IMAGE clone ids 2723592-2729326; 25% of the driver population), NCI-CGAP_Sub6 (pool Air-AU, IMAGE ids 2728969-2733190; 25% of the driver population), and NCI-CGAP_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described (Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG-LIB-NCI-CGAP_LuJ9

TAG-TISSUE-lung

TAG-SEQ-GACACG

BASE COUNT 190 a 154 c 160 g 192 t 1 others

ORIGIN

Query Match 28.5%; Score 643.2; DB 11; Length 697;

Best Local Similarity 97.7%; Pred. No. 2e-130; Matches 673; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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282 tcaggaccgcccgctcacttagtggcgaccctgaccacttgcctctggtccagtc 341
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697 tcaggaccgcccgctcacttagtggcgaccctgaccacttgcctctggtccagtc 638
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342 tcgataaattcgaagattggaagctcagtcgaggtcccccacagctgagtgctact 401
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637 tgcgataaattcgaagattggaagctcagtcgaggtcccccacagctgagtgctact 579
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402 gctgtggaacctgtgtaaaacacagtggtggttaaacctgggaataacatgaaagattctg 461
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462 tgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggggt 521
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518 tggagggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggggt 459
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522 accctgagcccgccgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 581
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458 accctgagcccgccgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 399
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398 acatgaagtcctcctcaccacacacacacacacacacacacacacacacacacacacacacac 339
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338 ctatgagcccttgcccaagcccaagcccaagcccaagcccaagcccaagcccaagcccaagcc 279
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278 ctcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 219
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158 ccaagatacaacaatacccaagatgctgctcctatcccatgaaagaatgctcagac 99
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98 atattgagaagaactactacaaagtggcatatactgcaatttaatttaattaaagata 39
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941 cctatttatatactctctatagaagaaa 969
|||||
38 cctatttatatactctctatagaagaaa 10
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RESULT 4
AUI38695 555 bp mRNA EST 25-OCT-2000

DEFINITION AUI38695 PLACE1 Homo sapiens cDNA clone PLACE1009110 5', mRNA sequence.

ACCESSION AUI38695

VERSION AUI38695.1 GI:11000216

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3951

Fax: 81-438-52-3952

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

Location/Qualifiers

1..555

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1b="PLACE1"

/tissue_type="placenta"

/note="Vector: PME18SFJ3"

BASE COUNT 151 a 126 c 129 g 145 t 4 others

ORIGIN

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Query Match 23.4%; Score 527.8; DB 10; Length 555;
Best Local Similarity 97.8%; Pred. No. 3.6e-105;
Matches 543; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
446 catgaaagattcttcggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggg 505
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61 catgaaagattcttcggtgggggtgggggtgggggtgggggtgggggtgggggtgggggtgggg 120
|||||
506 gtaactgcaagtgcttaccctgagcccgagcccgagcccgagcccgagcccgagcccgagccctata 565
|||||
121 gtaactgcaagtgcttaccctgagcccgagcccgagcccgagcccgagcccgagcccgagccctata 180
|||||
566 ggggtcagtagctctccacatgaaagtcctcctcactaccactgtgcaggaaggaagtggtg 625
|||||
181 ggggtcagtagctctccacatgaaagtcctcctcactaccactgtgcaggaaggaagtggtg 240
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626 tcatgagtcaggaatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 684
|||||
241 tcatgagtcaggaatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 300
|||||
685 cactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 744
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301 cactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 360
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745 ggtgtgagtcaggaagatggttcgagctcgaagaagataaagaataagtaggtatgctg 804
|||||
361 ggtgtgagtcaggaagatggttcgagctcgaagaagataaagaataagtaggtatgctg 420
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805 atccctctttaaagcccaagatacaatacccaagatgctgctcctatcccaag 864
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421 atccctctttaaagcccaagatacaatacccaagatgctgctcctatcccaag 480
|||||

```


QY	865	aaaaagggccatgacaaatlcttggaagaagcccctaacttcaagaagtgcataatgtcgaattta	924
Db	481	AAAAAGTGCATGACACTATTGGAMAANACCCTACTTCAAAGTGCCATYATATTGCAATTTA	540
QY	925	ttttaattaaaagat	939
Db	541	TTTTAATTAAAAGAT	555
RESULT	5		
AZ521126		AZ521126	467 bp DNA GSS 16-OCT-2000
LOCUS		RPCI-11-13K21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13K21	
DEFINITION		DNA sequence.	
ACCESSION		AZ521126	
VERSION		AZ521126.1	GI:10833636
KEYWORDS		GSS.	
SOURCE		human.	
TAXID		Homo sapiens.	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 467)	
AUTHORS		Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.	
TITLE		BAC end sequences of library RPCI-11	
JOURNAL		Unpublished (1997)	
COMMENT		Other_GSS: RPCI11-13K21.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhaoe@ig.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Plierer de Jong (pliererdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/) or from Research Genet cs (http://www.tigr.org/cdb/human/bac_end_search/bac_end_search.html) This BAC end was generated during the Rd process and may have higher chance of clone tracking errors. Seq primer: SP6 Class: BAC end.	
FEATURES		location/Qualifiers	
SOURCE		1..467	
		/organism="Homo sapiens"	
		/db_xref="GB:"750486"	
		/db_xref="taxon:9606"	
		/clone="RPCI-11-13K21"	
		/clone_lib="RPCI-11"	
		/sex="Male"	
		/cell_type="Lymphocytes"	
		/note=Vector: pBACS.6; Site_1: EcoRI; Site_2: EcoRI;	
		RPCI11 Human Male BAC Library"	
BASE COUNT		137 a 83 c 126 g 119 t	2 others
ORIGIN			
Query Match		20.6%; Score 465; DB 13; Length 467;	
Best Local Similarity		99.6%; Pred. No. 2e-91;	
Matches 465; Conservative		0; Mismatches 2; Indels 0; Gaps	
QY	1203	tgacctggttgtgtgttagtagtgatgaagaagaacagtcctcgacaagccaacggaagga	1262
Db	1	TGCTCTGTGTTGGTTGATGATCATCAGGAAGAATCGATCCACAAGGCCACTGACGACAGA	60
QY	1263	ggctgtgcTgaattgtgtgtgcTggaactcTctgtgTaaagaaactTaaagaaacaaatca	1322
Db	61	GGCTGTGCTCTGAGTTTGTGTGTCGTCGATGATCTCTGCTGGAAGCACTTAAGAACAAATAATCA	120
QY	1323	tcTgtgatcatcttctcagaagaalcaacagcccccttgagaltccaaggcatgtgaccagt	1382

Db	121	TCTGTAATTCCTTCTTGAGAGATCACAGCCCTCGNATTTCCAGGATTTGATTCAGT	180
Oy	1383	ctctaaagaagcctgcgtactggttgaatgylgtcccccataatcacaatcctcttgg	1442
Db	181	CTCTAAGAAGCCTGCTGACTGTTGTAATTTGTGCCCTCAATATTCACATCTCTTGG	240
Oy	1443	aatctcagctctgtgagttatttggagaagtaagtcctcgcagagtagttagttaagca	1502
Db	241	AATCTCACTCTGTGAGTTATTTTGGAGTAAGAGTCTTCGCGAGATCTACTTGTATTAAGCA	300
Oy	1503	aggtcatcctgagtaaggttagaccataatcacaatcagttcctcttctatgaagaag	1562
Db	301	AGGTCACTCTGTGATGAAGTATGAGCTTAATTCATATATACGTCTTCTTGTATGAAGAAG	360
Oy	1563	gagagagacacagagacagagagacgctggggaagaactatgtaagaatgaagcagaag	1622
Db	361	GAGAGACACAGACAGAGAGAGAGAGCGCGNAGAACTATGTAAGATGATGAAGCAGATC	420
Oy	1623	ggagatttgcagcccaagctaaagaaacacccaagatctgtggcaac	1669
Db	421	GGAGTTTGCAGCCACAAGCTAAGAAACACCAAGATTTGTGGCAAC	467

28-AUG-1998
 sapiens cDNA clone

adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

BASE COUNT 132 a 92 c 119 g 142 t
ORIGIN

Query Match 20.0%; Score 451.2; DB 10; Length 485;
Best Local Similarity 97.1%; Pred. No. 2e-88;
Matches 470; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Oy 487 gaatcattcctgcttaattgtaactgcagaagtgcttaccctgagcccgagcccaacca 546
Db 485 GAATCATTTCCCGTTAATGTAAGTACACGAGTGTACCTTGAGACCCCGAGGCAACCA 426
Oy 547 tcccaagttgagccttaagagtgatagctccacatgaatctctccactcaccact 606
Db 425 TCCCAAGTTGAGCCTTATAGGGTCAAGTCTCCACATGAACAGCCTGTCACTCAACACT 366
Oy 607 gtcgaagagagaggtgctcatagagtcagagatctatgccccttgcccgagccacc 666
Db 365 ATGCAGAGAGAGAGGTGCTATGAGACTCAAGGATCTATGGCCCTTGCCGACGCCACAC 306
Oy 667 cccctccctt-atccctgcaactgcatatgtaaccttccatctctccctcaccatc 725
Db 305 TCCCTCCCTTAAATCTGCGCACCTGCTATGCTACCTTCTCTCTCTCCCTCATCATC 246
Oy 726 ttgtgtgagagatagagaggtgagtgatgcagaagaatgctgcagcccgagcaagataa 785
Db 245 TTGTTTGCGGATAGAGAGGTGCTGATGTCAGAGAAATGCTGCGAGCTCAGAGATATA 186
Oy 786 agataagtaaggtatgctgacccctctttaaaccacagatacaatcaaatccagat 845
Db 185 AGATAAGTAGAGGTATGCTGATCCTCTTTTAAAAACCAAGATACATCAAAATCCAGAT 126
Oy 846 gctggtcctcttcccttgaaaaagtgctatgacatattgaaagaactactataaag 905
Db 125 GCTGCTCTATTCCTCCAGAAAGTCTCATGACATATGAGAAACACTACTTACAAAG 66
Oy 906 tgcacatattgcacatattttaaataaagaataaccatataatcttcttcttcttctt 965
Db 65 TGGCATATATGCAATTTATTTAATTAATAAAACCTACCCATATATTTCTTTATAGAA 6
Oy 966 aaaa 969
Db 5 AAAA 2

RESULT 7
B 74/c 464 bp mRNA EST 19-JAN-2001
LOCUS nab43f02.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:3268827 3', mRNA sequence.
ACCESSION BF435174
VERSION BF435174.1 GI:11447462
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 464)
NCL-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Glibco
High quality sequence stop: 461.
FEATURES
Location/Qualifiers
1..464

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3268827"
/clone_lib="Soares NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was from
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2H8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326653 Soares NBHOT
pool 1: 723720-726407, 739080-740999 subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 125 a 95 c 106 g 138 t
ORIGIN

Query Match 19.3%; Score 435.8; DB 11; Length 464;
Best Local Similarity 99.3%; Pred. No. 4.8e-85;
Matches 448; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 1803 accaagataattggttaacagcagctcttaagaaactaatacagctgctataaagtccct 1862
Db 464 ACCAAGATTAATTGGTTACAGCAGCTCTAGGAACATAACGCTGCTAAATGATCCCT 405
Oy 1863 gtccctccggtttacaattgtgtgtgtgtccctccacaaatgtaaccaagtgtccttg 1922
Db 404 GTCTCTCGTGTTTACATTCTGTGTGTGTCCCTCCCAATATGTACAAAGTGTGCTTTG 345
Oy 1923 tgacccaatagaatatgycagaagtgatgcatgacacttccaagaattaggtataaaag 1982
Db 344 TGA-CCAAATGAATATGAGCAGAGTATGCGATGCCATTCACAAAGTATGTTATAAAG 286
Oy 1983 acaattgagcttctacttgagccctctctctctgcacacccagcccccacatctcttg 2042
Db 285 ACACGTGACGCTTACTTGTGAGCCCTCTCTTGTGACACCCGCCGCCCAATCTATCTTG 226
Oy 2043 gctcactgcgtctgagggagcagctgacatgctatgagcagccctataaagaagacta 2102
Db 225 GCTCCTCGCTTGGGGAGAGCTAGCTGCCATGCTATGAGCAGGCCCTATTAAGAGACTTA 166
Oy 2103 cgtgtaaaaaatgaagttctctctgcccacagccacattagtgaaactagaagcagaagact 2162
Db 165 CGTGCTAAATAATGAAGTCTCTGCGCCACAGCCACATATGTAAGACTAGAACAGAGACT 106
Oy 2163 ctgtgagataatcgatgtgtgtgtttaaagtgctcagatgttggtctactactgtatgc 2222
Db 105 CTGTGAGATATATCATGCTTGTGTTTAAAGTTGCTACGTTTGTCTAAGTGTATATGC 46
Oy 2223 agcaatagataaataatcagagaagaag 2253
Db 45 AGCAATAGATTAATTAATATATGCAGAGAAAGAG 15

RESULT 8
A1831402/c 464 bp mRNA EST 21-DEC-1999
LOCUS A1831402
DEFINITION w364607.x1 NCL-CCAP_Lu19 Homo sapiens cDNA clone IMAGE:2407572 3',
mRNA sequence.
ACCESSION A1831402
VERSION A1831402.1 GI:5452073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 464)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrr/image/image.html
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 Seq primer: -400P from Gibco
 High quality sequence stop: 433.
 Location/Qualifiers

RES 1..464
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 /db_xref="taxon:9606"
 /clone="IMAGE:2407572"
 /clone_11b="NCI-CGAP_Lu19"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pPT73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 pooled lung tumor tissue, and was then primed with a Not I
 - oligo(dT) primer. Double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pPT73 vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.
 Fatima Bonaldo."

BASE COUNT 128 a 94 c 104 g 138 t
 ORIGIN

Query Match 18.9% Score 426.8; DB 10; Length 464;
 Best Local Similarity 98.2%; Pred. No. 4.5e-83;
 Matches 442; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Q 1804 ccaagataatgtgttcaagcagctctagaactaatacagctgtctaaatgaatccctg 1863
 |||||||
 Db 464 ccaagataatgtgttcaagcagctctagaactaatacagctgtctaaatgaatccctg 405
 |||||||
 Q 1864 tctctctgttctacatctgtgtgtgtccctcccaaatgataatgtctctgt 1923
 |||||||
 Db 404 tctctctgttctacatctgtgtgtgtccctcccaaatgataatgtctctgt 345
 |||||||
 Q 1924 gaccacaataatgtgacagaagtgatgcatgacctccaagattaggtatataaaga 1983
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 Db 344 gaccacaataatgtgacagaagtgatgcatgacctccaagattaggtatataaaga 286
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 Q 1984 caatgacgtcttactgtgagccctctctctgtgcaaccacacccccaatctatctg 2043
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 Db 285 caatgacgtcttactgtgagccctctctctgtgcaaccacacccccaatctatctg 226
 |||||||
 Q 2044 ctactgtgctctgtggaagtagtgcatagtatagagagagctataaagaacttac 2103
 |||||||
 Db 225 ctactgtgctctgtggaagtagtgcatagtatagagagagctataaagaacttac 166
 |||||||
 Q 2104 gtggtaaaaaatgaagtcctgcccacagacacattagtaacctagaacagagactc 2163
 |||||||
 Db 165 gtggtaaaaaatgaagtcctgcccacagacacattagtaacctagaacagagactc 106
 |||||||
 Q 2164 tctgagataatcgaatgttctgtttaaagttgctcagtttggcttaactgttatga 2223
 |||||||

Db 105 TGTGAGATAATCATGATGTTTGTGTTTAACTTGCTACATTGTCATACCTGTTATGCA 46
 Qy 2224 gcaatagataataatataatgacagagaagag 2253
 |||||||
 Db 45 GCAATAGATAATTAATATATGACAGAGAAGAG 16

RESULT 9
 LOCUS AI469873/c 442 bp mRNA EST 14-APR-1999
 DEFINITION U788a08.x1 Soares.NSF_F8_9W_OT_PA_P.S1 Homo sapiens cDNA clone
 IMAGE:2148566 3', mRNA sequence.
 ACCESSION AI469873
 VERSION AI469873.1 GI:4331963
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 442)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 Insert length: 610 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 437.
 Location/Qualifiers

1..442
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 /db_xref="taxon:9606"
 /clone="IMAGE:2148566"
 /clone_11b="Soares.NSF_F8_9W_OT_PA_P.S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pPT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and clones: Soares NBHSF pool 1:
 309384-310919, 323208-325895 Soares NB2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152337 Soares NB2HP8-9W pool 1:
 758280-760583, 772104-774407 Soares NBHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NBHOF
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 119 a 89 c 102 g 132 t
 ORIGIN

Query Match 18.5% Score 417; DB 10; Length 442;
 Best Local Similarity 99.8%; Pred. No. 6.2e-81;
 Matches 428; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Q 1825 agctctggaacataatacagctgtaaaatgataccctgtctcgtgttatactctg 1884
 |||||||
 Db 442 AGCTCTAGGAACATTAATACCTCTAAATGATCCCTGCTCCGCTTTAATCTTG 383
 |||||||
 Q 1885 tctgtccctcccaaatgtacaaagtgtctcttgcacccaatagaatcagcaga 1944
 |||||||
 Db 382 TGTGTGTCCTCCACAGATGTACCAAAAGTTGCTTTGTGA-CCAATAGATATAGGCGAGA 324
 |||||||
 Q 1945 agtgaatgcatgcaactccaagattaggtataaagaacacagctctactatgac 2004
 |||||||
 Db 323 AGTGATGCATGCCACTTCCAAAGATTAGGTTAAAGACACTGCACCTTACTTGAGC 264
 |||||||

QY 2005 cctctctctcgtccacccacccgcccccaatctatcttggctcactcgtctcgggggaagc 2064
|||||
Db 263 CCTCTCTGCTGTCACACCCGCCGCCCAATCTATCTTGGCTCACTCCGCTGGGGGAGC 204
QY 2065 tagctgcacatgctatgagcagggccataaagaagacttaagtggttaaaaatgaagctcc 2124
|||||
Db 203 TAGCTGCCATGCTATGACACGACCTATTAAGAGACTTACGCTTAAATAATGAAGTCTCC 144
QY 2125 tccccacacacacatagtgaaacctagaagacagagactctgtgataatcgaatggtt 2184
|||||
Db 143 TCCCCACAGCCCATTTAGTAACCTAGACAGACACTCTGTGATTAATCGATGTTTGT 84
QY 2185 tgttttaagttgcagttcttgcttaactgtctatgcaagaataga taaataatgca 2244
|||||
Db 83 TGTTTTAAGTCTCAGTTTGTGCTTAAGTCTTATGACGAATAATGAATATATATGCA 24
QY 2245 gaggaaagag 2253
|||||
Db 23 GAGAAAGAG 15

RESULT 10
LOCUS B1089828 726 bp mRNA EST 20-JUN-2001
DEFINITION 60285507JF1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:496432 5',
mRNA sequence.
ACCESSION B1089828
VERSION B1089828.1 GI:14508158
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 726)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM1021 row: n column: 17
High quality sequence stop: 709.
Location/Qualifiers
1. 726
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:496432"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/note="Host="DH108"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 151 a 201 c 213 g 161 t
ORIGIN

Query Match 18.4% Score 413.8; DB 11; Length 726;
Best Local Similarity 96.9%; Pred. No. 3e-80;
Matches 443; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1 aatccaagagctcacctctacacgagcgagacatgagggctcaactcagctcagtcgagcg 60
|||||
Db 271 ATCCAGAGCTTCACTTCTACCGCGGACATGGGGCTCACCCTCCAGCTTCGAGTCGG 330

QY 61 ctgctaccggygctggtctcgtgcaaggtgctgaagccgaatcagctctcagactca 120
|||||
Db 331 CTGCTACCCGGGCTGGTCTCTGTGCACGGTGCCTGAAGCCGATCAGCTGTGACACTCA 390
QY 121 cccagctcccggaagatggtgctggaatgcccccaatcaagaagcttctacttcagcaat 180
|||||
Db 391 CCCAGCTTCCGAGAAAGTGTCGGAATGCCCCCAACACAGACTTCTACTTCCACCACT 450
QY 181 gtgaatgagcaagctgccccccagaaacccctcctggaagcagagcagctgggtgaaggt 240
|||||
Db 451 GTGACTAGGGAACAGTGC -CCCCCAGAACTCCCTGGGCAAGCCAGCTCGGGTGAAGGT 509
QY 241 gagtgaagagaccatagtcggagcaatcactcttctgctctcgaagaccacccagtcga 300
|||||
Db 510 GAGTGAGAGAACCCAGTGGCGGACATCATCTCTGCTCAGGACCCCGACGTCTGA 569
QY 301 cttagtggaccccgacacacttctcttctggttccagtttgcataaatctcgaatct 360
|||||
Db 570 CTTACTGGGACACTGACACACTTGTCTGTCGTCGCCAGTATGGAATATTCGAGATTTT 629
QY 361 gagctcagtcacaggtcct -ccccacatgatatgtctactgtctgtgaacctgtgaa 419
|||||
Db 630 GAGCTCAGTCCACGCTGCTACCCCACTGGATGCTCTGCTGTGACACTTGTAA 689
QY 420 aaccatgtggtggttaacttggaataacatgaagaat 456
|||||
Db 690 AACCATGTGGGTAAACTGGGAATCACCCTGAAAGAT 726

RESULT 11
LOCUS AL545100 932 bp mRNA EST 16-FEB-2001
DEFINITION AL545100 LTI_NFL006_P12 Homo sapiens cDNA clone CS0D1013YA07 5
prime, mRNA sequence.
ACCESSION AL545100
VERSION AL545100.1 GI:12677581
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 932)
L.I.W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 932
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1013YA07"
/clone_lib="LTI_NFL006_P12"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site: 1; NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 206 a 230 c 290 g 201 t
ORIGIN

Query Match 17.9% Score 404; DB 10; Length 932;
Best Local Similarity 94.4%; Pred. No. 4.2e-78;
Matches 459; Conservative 3; Mismatches 18; Indels 6; Gaps 4;

```
QY 1 aatccaaagagcttacccttaccgagcagatgagggctcaccctcagcttcgagtcg 60
D 375 AATCCAAAGAGCTTACCTTCTACCGCGCGGACATGGGCTCACCCTCCAGCTTCGAGTGG 434
QY 61 ctgctaccacccggagcttggctcctgctgcacagtgctcgaagccgacgctgctcagactca 120
D 435 CTGCTACCCCGGGCTGGTCTGTGACAGGCTGCTGAAAGCCGATCAGCTGTGACAGTCA 494
QY 121 cccagcttcccgagaatgagtgctggaatgcgcccaatcacagacttctacttccagcagt 180
D 495 CCCAGCTTCCCGAGAAATGCTGGATGCCCCATCACAGACTTCTACTTCCAGCAGT 554
QY 181 gtgactgaggaagctgccccccagaaactcctcggagagagcagcagcgggtgagaggt 240
D 555 GTGACTAGGAGCAAGCTG-CCCCCAGAACTCCTGGGAGAGCCAGCTGGGAGGAGGT 613
QY 241 gagtggaggaagaccatgagcgaacatcactcttctgctcagagaccccgagctcga 300
D 614 GAGTGGAGAGACCCCATGGCGGACATCATCTCTCTCTCTCAAGAGACCCCGAGTCTGA 673
QY 301 ctgagtgagcactgacacacttctctctgctcagcttgcataaattcagagatt 360
D 674 CTGAGTGGGCA-CTGACCATTTGCTTCTGCTCCAGTTGGATTAATCTGAGATT 732
QY 361 ggaactcagagcagagctccctcccaactgagtgctgctgctgctgagacctgtaaaa 420
D 733 GGACTCAGTCCAGCGTCTCCCTCCACTGATGGTGTCTACTGCTGTGGAACCTTGT-AAA 791
QY 421 accatgtggggtaaacctggaataacatgaaaagattctgtgggggtgggggtggag 480
D 792 ACCATGTGGGGTAACTGGGATTA--TGAAAGATTCTGTGGGGGTGGGGGGGRT 848
QY 481 tgcctg 486
D 849 GGTGGG 854
^ Db 849 GGTGGG 854

RESULT 12
LOCUS AA722902 414 bp mRNA EST 02-JAN-1998
DEFINITION 2881a03.s1 Soares_fetal_heart_NDHH19W Homo sapiens CDNA clone
IMAGE:399724 3', mRNA sequence.
ACCESSION AA722902
VERSION AA722902.1 GI:2740609
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,
Kitzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,
J., Moore,B., Scheinberg,K., Stepien,M., Tan,F., Theisling,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
JOURNAL Mashu-NCI human EST Project
COMMENT Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 401.
FEATURES
SOURCE Location/Qualifiers
1..414
/organism="Homo sapiens"
/db_xref="GDB:1307547"
/db_xref="taxon:9606"
/clone="IMAGE:399724"
```

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/clone_id="Soares_fetal_heart_NDHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pRT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGGAGCGGCGGACCTCTTTTCTTTTCTTTTCTTTT
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHH19W."
```

BASE COUNT 119 a 83 c 98 g 114 t

ORIGIN

Query Match 17.7%; Score 398.2; DB: 10; Length 414;
Best Local Similarity 99.0%; Pred. No. 8.1e-77;
Matches 411; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
QY 1833 gaaactaatcagctgctcaaatgatccctgctcctcctgcttctacattcgtgtgtc 1892
D 414 GAACTAATACAGCTGCTAAATGATCCCTGTCTCTGTTTACATCTCTGTGTGTC 355
QY 1893 cctccccacaaatgacaaatgctcctgctgacccaaatgaaatgagaaatgagatg 1952
D 354 CCTCCACCAATGTACCAAAATGCTTGTGTGTA-CCAATAGAAATGCGCAAGATGATG 296
QY 1953 catgcaacttccaagattagttataaagacactgcagcttctacttgaaacctcttc 2012
D 295 CATGCCACTTCCAGATTAGGTATTAAGAACACTGCAGCTTCTACTGTGACCCCTCTTC 236
QY 2013 tctgcaaccacccgcccccaatctatcttgcctcactgcctcctgaggagacagctgccc 2072
D 235 TCTGCCACCCACCGCCCATATCTATCTTGCTGCTACTGCTGTGGGGAACACTGCTCC 176
QY 2073 atgctatgagcagcctataaagagactacgtgtgtaaaaaatgaagctcctccaca 2132
D 175 ATGCTATGAGCAGCGCTTAAAGAGACTTATGTGTAATAAATGAAGTCTCTCCACCA 116
QY 2133 gccacatagtgtaacctgaagcagagactctgtagaataatcgattgtgttttaa 2192
D 115 GCCACATTAGTGAACCTTGAAGCAGAGACTGTGATATCAATGTTGTGTTTAA 56
QY 2193 gtgctcagcttgcctcaactgtgtatgcagcaataaataatgagag 2247
D 55 GTTGCTAGTTTGTGCTACTTGTATGACAGCAATACATAATATATGTCAGAG 1
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RESULT 13
LOCUS BE711845 435 bp mRNA EST 12-SEP-2000
DEFINITION QV2-HIT0698-070700-264-h07 HIT0698 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE711845
VERSION BE711845.1 GI:10100110
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zaio,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

QY	801	gcgtatccctctttaaataaccaagatatacaataaataccagatgctgctcctatcc	860
Db	170	gctatccctctttaaataaccaagatatacaataaataccagatgctgctcctatcc	111
QY	861	catgaataagtcgcatagcatacttgaagaacctactcaagaatgcgcataatgcga	920
Db	110	catgaataagtcgcatagcatacttgaagaacctacttgcgaatgcgcataatgcga	51
QY	921	ttcatcttaattaaagaatacctaattatataatctcttaataagaataa	969
Db	50	tttatatttaattaaagaatacctaattatataatctcttaataagaataa	2

RESULT	15								
LOCUS	AU157708/c								
DEFINITION	AU157708	416 bp	mRNA						
VERSION	AU157708								
KEYWORDS	AU157708.1	GI:11019229							
SOURCE	Est.								
	human.								

REFERENCE
Oota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawal, Y.,
1 (bases 1 to 416)
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo..
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

TITLE	H1I human CDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Salto,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,T., Nagai,T., Sugano,S., Isogai,T.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES	Location/Qualifiers
source	1. .416

BASE COUNT	ORIGIN
118 a	13 others
86 c	82 g
117 t	

Query Match	16.9%	Score 380.8	DB 10	Length 416
Best Local Similarity	95.0%	Pred. No. 5.2e-73		
Matches 396	Conservative	0	Mismatches 20	Indels 1
				Gaps 1

OY	1835	aactcaatacagctgcgtctaaatgtaaccctgctctccctgcgtgttacaattctgtgltccc	1894
Db	416	AAATAATACAGNGNTAAAANGATCCNTGNTCTTGGTATACACTTCGTGTGTGCC	357
OY	1895	ctcccaacaatgtaccaaagtgtcctctgtgacccaataaataatgycagaagtgtatgca	1954
Db	356	CTCCACACATGTACCAAAAGTTGTTTGTGCA-CCAAATGAATAATGGCAGAAATGATGCGCA	298
OY	1955	tgcacattccaagatttggtataaagaacatgcagccttcaacttggacccctctctc	2014
Db	297	TGCCACTTCCAAGTTTGGGTTATAAAAGACACGACAGNTTTACTTGACCCCTNTTTTTTN	238

OY	2015	tgtaaccacacgcccccaatcctctgtgctaacctgcgcctccggggggaucctagcttgcacat	2074
Db	237	tgccaccaccacgcccaccaatnntatcttgctgctacctgcctctg6gggaaactagctgcacat	178
OY	2075	gcta.tgacgaagcctctaagaagacttaccgtg.taaaaaa.tgaagtcctctc.tgccacagc	2134
Db	177	gctatmgacgacgacctatnnaagagacttacctggtataaaaatgaagntcctccacacagc	118
OY	2135	cacattag.tgaaccttagaagcagagactcctg.vagata.taatcga.tgcttctgttcttaagc	2194
Db	117	cacatttagtgtaacctgaacacacagcagantctgtgagatnntcga.tgttgcttttttaagt	58
OY	2195	tgcccgagtttctgctactactctgtat.tgacgcaat.tagaataa.taatat.tgaaggaag	2251
Db	57	tgcctcagtttttgcttactctgtttatgcacacatnntaatnntatnntgcaggaag	1

Search completed: March 1, 2002, 11:23:51
Job time: 4097 sec

